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 Napier, Mary A.  
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Tyr	Ser	Asp	Leu	Gly	Tyr	Tyr	Ile	Ile	Asn	Lys	Leu	His	His	Val					
				110					115					120					
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu					
				125					130					135					
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly					
				140					145					150					
Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser					
				155					160					165					
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu					
				170					175					180					
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu					
				185					190					195					
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu					
				200					205					210					
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly					
				215					220					225					
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe					
				230					235					240					
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg					
				245					250					255					
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser					
				260					265					270					
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val					
				275					280					285					
Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr					
				290					295					300					
Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr					
				305					310					315					
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val					
				320					325					330					
Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr					
				335					340					345					

Pro Asn Val Ser Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val	Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg	Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser	Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val	Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp	Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu	Glu Asn Glu	485	490	

<210> 8  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 33, 66, 96, 387  
 <223> unknown base

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 tgagcttctg gtgccntttg gctctaattc tggccacaca gagaancagt 100  
 cggcctaattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
 tgccatacgg ctgggtgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
 ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcagc 350  
 tctgtttcgt gatgttttg acaccaacg tgtctgngaa aatcttgata 400  
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttcottt 450

gcggatcttc tcctttctcc cagttccagt cacagtgagg gcgcattctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273, 293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggctggg tctcctgggt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgtnt gtttcgtgat 150

gttttgga cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgagaa ntttgnngtg ttcctttgcg gattttctcc 250

tttttccag ttccagtcac agngagggcg catctaccg gnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcttac cctacctggg ggtgcacggt 400

gcgacctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

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agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 11  
 ctgatccggt tcttggtgcc cctg 24

<210> 12  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 12  
 gctctgtcac tcacgctc 18

<210> 13  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 13  
 tcatctcttc cctctccc 18

<210> 14  
 <211> 18  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 14  
 ccttcgcgca cggagttc 18

<210> 15  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 15  
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<210> 16  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
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<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

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ctctgcccc tgcattcctgt gcagctgtgt ccccgccagc cgcaactcca 150  
ccgtgagccg cctcatcttc acgtttcttc tcttcctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350  
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gctgcaggcc tcggctcatca cctctacac catgtttgtc acctggtcag 900  
ccctatccag tatcctgaa cagaaatgca accccattt gccaaaccag 950



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 cagaccgagg agtgcacacc tatgctagac gccacacagc agcagcagca 1150  
 gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
 tcacctacag ctactccttc ttccacttct gcctggtgct ggcctcactg 1250  
 cacgtcatga tgacgtcac caactggtac aagcccggtg agaccggaa 1300  
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
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 tggtcacgtc cccaggggga cctgcccc ttcttggaact tcgtgcctta 1850  
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a 1901

<210> 19  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

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 1 5 10 15  
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
 20 25 30  
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
 35 40 45  
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
 50 55 60

Val	Glu	Ser	Gln	Leu 65	Tyr	Lys	Leu	Pro	Trp 70	Val	Cys	Glu	Glu	Gly 75
Ala	Gly	Ile	Pro	Thr 80	Val	Leu	Gln	Gly	His 85	Ile	Asp	Cys	Gly	Ser 90
Leu	Leu	Gly	Tyr	Arg 95	Ala	Val	Tyr	Arg	Met 100	Cys	Phe	Ala	Thr	Ala 105
Ala	Phe	Phe	Phe	Phe 110	Phe	Phe	Thr	Leu	Leu 115	Met	Leu	Cys	Val	Ser 120
Ser	Ser	Arg	Asp	Pro 125	Arg	Ala	Ala	Ile	Gln 130	Asn	Gly	Phe	Trp	Phe 135
Phe	Lys	Phe	Leu	Ile 140	Leu	Val	Gly	Leu	Thr 145	Val	Gly	Ala	Phe	Tyr 150
Ile	Pro	Asp	Gly	Ser 155	Phe	Thr	Asn	Ile	Trp 160	Phe	Tyr	Phe	Gly	Val 165
Val	Gly	Ser	Phe	Leu 170	Phe	Ile	Leu	Ile	Gln 175	Leu	Val	Leu	Leu	Ile 180
Asp	Phe	Ala	His	Ser 185	Trp	Asn	Gln	Arg	Trp 190	Leu	Gly	Lys	Ala	Glu 195
Glu	Cys	Asp	Ser	Arg 200	Ala	Trp	Tyr	Ala	Gly 205	Leu	Phe	Phe	Phe	Thr 210
Leu	Leu	Phe	Tyr	Leu 215	Leu	Ser	Ile	Ala	Ala 220	Val	Ala	Leu	Met	Phe 225
Met	Tyr	Tyr	Thr	Glu 230	Pro	Ser	Gly	Cys	His 235	Glu	Gly	Lys	Val	Phe 240
Ile	Ser	Leu	Asn	Leu 245	Thr	Phe	Cys	Val	Cys 250	Val	Ser	Ile	Ala	Ala 255
Val	Leu	Pro	Lys	Val 260	Gln	Asp	Ala	Gln	Pro 265	Asn	Ser	Gly	Leu	Leu 270
Gln	Ala	Ser	Val	Ile 275	Thr	Leu	Tyr	Thr	Met 280	Phe	Val	Thr	Trp	Ser 285
Ala	Leu	Ser	Ser	Ile 290	Pro	Glu	Gln	Lys	Cys 295	Asn	Pro	His	Leu	Pro 300
Thr	Gln	Leu	Gly	Asn 305	Glu	Thr	Val	Val	Ala 310	Gly	Pro	Glu	Gly	Tyr 315
Glu	Thr	Gln	Trp	Trp 320	Asp	Ala	Pro	Ser	Ile 325	Val	Gly	Leu	Ile	Ile 330
Phe	Leu	Leu	Cys	Thr 335	Leu	Phe	Ile	Ser	Leu 340	Arg	Ser	Ser	Asp	His 345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met

350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu		
365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr		
380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met		
395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met		
410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp		
425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu		
440	445	450
Leu Arg Asn Arg Asp Phe Ser		
455		

- <210> 20
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 20
- gccgcctcat cttcacgttc ttcc 24
- <210> 21
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 21
- tcatccagct ggtgctgctc 20
- <210> 22
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 22
- cttcttccac ttctgcctgg 20
- <210> 23
- <211> 18



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ttggcaaaga tgaacagcag agaatttcaa aggacottgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
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cgaggcttca ttcgttatgg ctggcgctgg gggtggagaa ctgcagtgtt 600  
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gtactotcac tttacttate cttaaattta aatacatact tatgtttgta 1250  
ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
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t 1351

<210> 28  
<211> 285  
<212> PRT  
<213> Homo sapiens

<400> 28  
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Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcatg gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 262, 330, 371  
 <223> unknown base

<400> 30  
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 gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
 cttgtgtgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
 agagccaggc agaaatttat nataacc 377

<210> 31  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 31  
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<210> 32  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 34  
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<210> 35  
<211> 1819  
<212> DNA  
<213> Homo sapiens

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ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100  
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tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200  
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250  
gctaattgga attgctgcgt ggggcattgg cttogggctg atttccagtc 300  
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tttttatatg attattctgt tacttgtatt tattgttcag tttctgtat 450  
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500  
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gaatatgctg gagaggtttt gagatttgtt ggtggcattg gcctgttctt 700



cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750  
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 gaagatttcc ttctgtatta tgatcttggt cactttctgt aattttctgt 850  
 taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900  
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 ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050  
 cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100  
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 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350  
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 atctcccata atttgaaatt gaaatcgtat tgtgtgggtc tgtatatatt 1750  
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 taaaagaaag taatggaag 1819

<210> 36  
 <211> 204  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile  
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gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350

gacacctgggt gtttggtga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

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tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250  
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ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcataattga atatgatctc ccataatttg aaattgaaat cgtatttgt 500  
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gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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tggttggtcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggtctngctg tggtaaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

accacagtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

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 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgcctt 2000  
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 ttgtagccta a 2061

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 <211> 359  
 <212> PRT  
 <213> Homo sapiens

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 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 47  
 tttccagcgc caattctc 18

<210> 48  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 48  
 agttcttgga ctgtgatagc cac 23

<210> 49  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 49  
 aaacttggtt gtcctcagtg gctg 24

<210> 50  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 50  
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<210> 51  
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 <212> DNA  
 <213> Homo sapiens

<400> 51  
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 gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcttggg 150  
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<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
 35 40 45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
 80 85 90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
 95 100 105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
 110 115 120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
 125 130 135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
 140 145 150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
 155 160 165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180

Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr	185	190	195
Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe	200	205	210
Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile	215	220	225
Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys	230	235	240
Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser	245	250	255
Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr	260	265	270
Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe	275	280	285
Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr	290	295	300
Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His	305	310	315
Val Tyr Glu Ala Ala Arg	320		

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic oligonucleotide probe  
  
 <400> 53  
 tatccctcca attgagcacc ctgg 24  
  
 <210> 54  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic oligonucleotide probe  
  
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 <210> 55  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

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cgataatgaa gggaaccaa aagtggatg cacttactcc agtcgtcatg 400

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<210> 59  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
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 Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys  
                     20                    25                    30  
 Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp  
                     35                    40                    45  
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln  
                     50                    55                    60  
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
                     65                    70                    75  
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
                     80                    85                    90  
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
                     95                    100                    105  
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
                     110                    115                    120  
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
                     125                    130                    135  
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
                     140                    145                    150  
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
                     155                    160                    165  
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro  
                     170                    175                    180

09072295 101501

Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
Ser	Met	Ile	Pro	Ser	Gln	Ser	Arg	Ala	Phe	Gln	Thr	Val			365	370	

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61  
actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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tctccccgcc tggggcgccct cgccgctggg cagggtgctga gcgcccctag 150  
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 <211> 655  
 <212> PRT  
 <213> Homo sapiens

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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu  
 20 25 30

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				35					40					45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
				110					115					120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
				260					265					270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
				275					280					285	
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
				290					295					300	
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
				305					310					315	
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	

320	325	330
Pro Lys Arg Gly His 335	Pro Arg Gln Asn Leu His Lys His Phe Asp 340	345
Ile Asn Glu His Leu 350	Pro Trp Met Ile Val Leu Phe Leu Leu Leu 355	360
Val Leu Val Val Ile 365	Val Val Cys Ser Ile Arg Lys Ser Ser Arg 370	375
Thr Leu Lys Lys Gly 380	Pro Arg Gln Asp Pro Ser Ala Ile Val Glu 385	390
Lys Ala Gly Leu Lys 395	Lys Ser Met Thr Pro Thr Gln Asn Arg Glu 400	405
Lys Trp Ile Tyr Tyr 410	Cys Asn Gly His Gly Ile Asp Ile Leu Lys 415	420
Leu Val Ala Ala Gln 425	Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln 430	435
Phe Leu Cys Asn Ala 440	Ser Glu Arg Glu Val Ala Ala Phe Ser Asn 445	450
Gly Tyr Thr Ala Asp 455	His Glu Arg Ala Tyr Ala Ala Leu Gln His 460	465
Trp Thr Ile Arg Gly 470	Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser 475	480
Ala Leu Arg Gln His 485	Arg Arg Asn Asp Val Val Glu Lys Ile Arg 490	495
Gly Leu Met Glu Asp 500	Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala 505	510
Leu Pro Met Ser Pro 515	Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser 520	525
Pro Asn Ala Lys Leu 530	Glu Asn Ser Ala Leu Leu Thr Val Glu Pro 535	540
Ser Pro Gln Asp Lys 545	Asn Lys Gly Phe Phe Val Asp Glu Ser Glu 550	555
Pro Leu Leu Arg Cys 560	Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu 565	570
Ser Arg Asn Gly Ser 575	Phe Ile Thr Lys Glu Lys Lys Asp Thr Val 580	585
Leu Arg Gln Val Arg 590	Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe 595	600
Asp Asp Met Leu His 605	Phe Leu Asn Pro Glu Glu Leu Arg Val Ile 610	615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu  
620 625 630

Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp  
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
650 655

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<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
gtagcagtgc acatggggtg ttgg 24

<210> 66  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 66  
accgcacatc ctcaagtctct gtcc 24

<210> 67  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 67  
acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68  
<211> 2412  
<212> DNA  
<213> Homo sapiens

<400> 68  
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tgtcagaggt cctgaaatag tcaccatggg ggaaaatgat ccgcctgctg 150  
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 catccactga aa 2412

<210> 69  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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 35 40 45  
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile  
 50 55 60  
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly  
 65 70 75  
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala  
 80 85 90  
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr  
 95 100 105  
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

05978285 101501

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Thr Ala Ala Ser Trp Lys Thr Met Cys	Ser Asp Asp Trp Lys Gly	
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr	
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe	
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys	
170	175	180
Val Thr Ala Leu His His Ser Val Tyr	Val Arg Glu Gly Cys Ala	
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg	
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu	
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His	
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala	
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile	
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His	
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg	
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr	
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu	
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala	
335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	
395	400	405



Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg  
425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp  
440 445 450

Leu Lys Thr

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<220>  
<223> Synthetic oligonucleotide probe

<400> 70  
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<210> 71  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 71  
tacacgtccc tgtggttgca gatc 24

<210> 72  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 72  
cgttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73  
<211> 3305  
<212> DNA  
<213> Homo sapiens

<400> 73  
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attgcaacgg tcaaggctgg cttgtgccag aacggcgcgc gcgcgcgcac 100  
gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp  
 50 55 60  
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu  
 65 70 75  
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile  
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 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly  
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 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys  
 125 130 135  
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val  
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 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro  
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 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His  
 170 175 180  
 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser  
 185 190 195  
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr  
 200 205 210

Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly Met	395	400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His Ser			

09978295 101501

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Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	
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His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	
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Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	
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Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	
680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln	
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro	
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile	
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<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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 ctaccagga agtttgaga aacagtgcaa ggaagggcag ganttcctgg 150  
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 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
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<210> 77  
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<400> 77  
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<210> 78  
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<220>  
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<400> 78  
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<210> 79  
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105401"5523/550

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
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<210> 80  
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<400> 80  
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<210> 81  
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<400> 81  
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<210> 82  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
cttcgctggg aagagtttg 19

<210> 83  
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<212> DNA  
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<210> 84  
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<212> DNA  
<213> Homo sapiens

<400> 84  
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<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 85  
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Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
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<210> 86  
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<220>  
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<400> 86  
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<210> 87  
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<400> 87  
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<210> 88  
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 88

gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89

<211> 2956

<212> DNA

<213> Homo sapiens

<400> 89

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
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 50 55 60  
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
 65 70 75  
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
 80 85 90  
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
 95 100 105  
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
 110 115 120  
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
 125 130 135  
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 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
 155 160 165  
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Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	
				200					205					210	
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	
				215					220					225	
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	
				230					235					240	
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	
				245					250					255	
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	
				260					265					270	
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	
				275					280					285	
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	
				290					295					300	
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	
				305					310					315	
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	
				320					325					330	
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
				335					340					345	
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
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His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
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<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



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gagaactggg tgatatggga gatcagggca atattggcaa gactggggccc 300  
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agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400  
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aaaaaaaaaa aaaaaa 1016

<210> 97  
<211> 277  
<212> PRT  
<213> Homo sapiens

<400> 97  
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20 25 30  
Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
35 40 45  
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
50 55 60  
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
65 70 75  
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys



05978235 "101501"

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				95					100					105					
Leu	Gly	Ile	Pro	Gly	Glu	Lys	Gly	Lys	Ala	Gly	Thr	Val	Cys	Asp					
				110					115					120					
Cys	Gly	Arg	Tyr	Arg	Lys	Phe	Val	Gly	Gln	Leu	Asp	Ile	Ser	Ile					
				125					130					135					
Ala	Arg	Leu	Lys	Thr	Ser	Met	Lys	Phe	Val	Lys	Asn	Val	Ile	Ala					
				140					145					150					
Gly	Ile	Arg	Glu	Thr	Glu	Glu	Lys	Phe	Tyr	Tyr	Ile	Val	Gln	Glu					
				155					160					165					
Glu	Lys	Asn	Tyr	Arg	Glu	Ser	Leu	Thr	His	Cys	Arg	Ile	Arg	Gly					
				170					175					180					
Gly	Met	Leu	Ala	Met	Pro	Lys	Asp	Glu	Ala	Ala	Asn	Thr	Leu	Ile					
				185					190					195					
Ala	Asp	Tyr	Val	Ala	Lys	Ser	Gly	Phe	Phe	Arg	Val	Phe	Ile	Gly					
				200					205					210					
Val	Asn	Asp	Leu	Glu	Arg	Glu	Gly	Gln	Tyr	Met	Ser	Thr	Asp	Asn					
				215					220					225					
Thr	Pro	Leu	Gln	Asn	Tyr	Ser	Asn	Trp	Asn	Glu	Gly	Glu	Pro	Ser					
				230					235					240					
Asp	Pro	Tyr	Gly	His	Glu	Asp	Cys	Val	Glu	Met	Leu	Ser	Ser	Gly					
				245					250					255					
Arg	Trp	Asn	Asp	Thr	Glu	Cys	His	Leu	Thr	Met	Tyr	Phe	Val	Cys					
				260					265					270					
Glu	Phe	Ile	Lys	Lys	Lys	Lys													
				275															

<210> 98  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 98  
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<210> 99  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccataacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctecatggc tgccctcctg ctgctgcccc tgctgctgtt gctaccgctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggtt cttcgagctc 400

gcgccctggc cgcggctgcc gccgaaccgg aaggtccga ggggggctgc 450

agcctggcct ggcgctcgc ggaactggcc cagcagcgcg ccgcgcacac 500

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 gaccttcaa cagcagaaag ttcggatggc aaatgagggc ttcgaccca 2200  
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 catggcccaa cttgtttatt gcag 2574

<210> 102  
 <211> 730  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
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 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala  
 35 40 45  
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu  
 50 55 60  
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp  
 65 70 75  
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys  
 80 85 90  
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro  
 95 100 105  
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu  
 110 115 120  
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser  
 125 130 135  
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala  
 140 145 150  
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp  
 155 160 165  
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala  
 170 175 180  
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe  
 185 190 195  
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro  
 200 205 210

Leu Ser Pro Gly Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly Pro	215	220	225
Glu Phe Leu Trp Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu Arg	230	235	240
Thr Ala Phe Val Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu His	245	250	255
Cys Leu Arg Ser Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro Glu	260	265	270
Phe Leu Glu Ser Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala Met	275	280	285
Gly Leu His Leu Trp Ala Ala Gly Pro	Gly Thr His Pro Ala Gly	290	295	300
Ile Ser Asp Leu Leu Ala Glu Val Ser	Ala Glu Val Asp Gly Pro	305	310	315
Val Pro Gly Tyr Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr Cys	320	325	330
Leu Tyr Ile Phe Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala Ala	335	340	345
Arg Ile Ser His Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr Gln	350	355	360
Leu Cys Gly Val His Gln Glu Asp Val	Ile Tyr Leu Ala Leu Pro	365	370	375
Leu Tyr His Met Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys Met	380	385	390
Gly Ile Gly Ala Thr Val Val Leu Lys	Ser Lys Phe Ser Ala Gly	395	400	405
Gln Phe Trp Glu Asp Cys Gln Gln His	Arg Val Thr Val Phe Gln	410	415	420
Tyr Ile Gly Glu Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro Ser	425	430	435
Lys Ala Glu Arg Gly His Lys Val Arg	Leu Ala Val Gly Ser Gly	440	445	450
Leu Arg Pro Asp Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly Pro	455	460	465
Leu Gln Val Leu Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val Ala	470	475	480
Thr Ile Asn Tyr Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala Ser	485	490	495
Trp Leu Tyr Lys His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr Asp			

500										505					510				
Val	Thr	Thr	Gly	Glu	Pro	Ile	Arg	Asp	Pro	Gln	Gly	His	Cys	Met					
				515					520					525					
Ala	Thr	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Leu	Val	Ala	Pro	Val	Ser					
				530					535					540					
Gln	Gln	Ser	Pro	Phe	Leu	Gly	Tyr	Ala	Gly	Gly	Pro	Glu	Leu	Ala					
				545					550					555					
Gln	Gly	Lys	Leu	Leu	Lys	Asp	Val	Phe	Arg	Pro	Gly	Asp	Val	Phe					
				560					565					570					
Phe	Asn	Thr	Gly	Asp	Leu	Leu	Val	Cys	Asp	Asp	Gln	Gly	Phe	Leu					
				575					580					585					
Arg	Phe	His	Asp	Arg	Thr	Gly	Asp	Thr	Phe	Arg	Trp	Lys	Gly	Glu					
				590					595					600					
Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp					
				605					610					615					
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His					
				620					625					630					
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His					
				635					640					645					
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu					
				650					655					660					
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu					
				665					670					675					
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn					
				680					685					690					
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu					
				695					700					705					
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr					
				710					715					720					
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile										
				725					730										

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 104  
 ggagaatgtg gccacaac 18

<210> 105  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 105  
 gccctggcac agtgactcca tagacg 26

<210> 106  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 106  
 atccacttca gcggacac 18

<210> 107  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 107  
 ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
 <211> 2579  
 <212> DNA  
 <213> Homo sapiens

<400> 108  
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 acgcgcgcat acacactcgc tctcgcttgt ccatctccct cccgggggag 150  
 ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgcg 200

gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250  
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 gcagtccaga gggctgcgct gctcgctccc tcggctggca gaaggggggtg 450  
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 cctgctccag ccctcagatc tgcccgctca gctcctgaaa attttaatac 1650



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 gacagcgggc acgtccaacg aggaggaatg ctggaacggg cacagcaaag 1850  
 ccagatactt gcctgagatc atgaatgatg ggctcaccaa ccagatcaac 1900  
 aatcccgagg tggatgtgga catcactcgg cctgacactt tcatcagaca 1950  
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 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500  
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<210> 109  
 <211> 555  
 <212> PRT  
 <213> Homo sapiens

<400> 109  
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 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
 65 70 75



365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu		
380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr		
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu		
410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile		
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp		
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met		
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly		
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser		
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe		
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Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg		
515	520	525
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

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<223> Synthetic oligonucleotide probe

<400> 112

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<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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<212> PRT  
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35 40 45  
Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
50 55 60  
Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
65 70 75  
Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
80 85 90  
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
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Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro







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<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086  
<223> unknown base

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Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
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Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
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Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300
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320	325	330
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<400> 121  
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<210> 122  
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 35 40 45  
 Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 127

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<223> Synthetic oligonucleotide probe

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<211> 23

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<223> Synthetic oligonucleotide probe

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<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 130

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<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131



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 tgttacaaaa taaaa 2365

<210> 132  
 <211> 571  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
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 Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys  
                     20                    25                    30  
 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
                     35                    40                    45  
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
                     50                    55                    60  
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
                     65                    70                    75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val		80	85	90
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu		95	100	105
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu		110	115	120
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro		125	130	135
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu		140	145	150
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln		155	160	165
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly		170	175	180
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu		185	190	195
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn		200	205	210
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met		215	220	225
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly		230	235	240
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp		245	250	255
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu		260	265	270
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp		275	280	285
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro		290	295	300
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly		305	310	315
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp		320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly		335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys		350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly				

365	370	375
Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly		
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Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu		
395	400	405
Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys		
410	415	420
Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp		
425	430	435
Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln		
440	445	450
Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu		
455	460	465
His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met		
470	475	480
Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu		
485	490	495
Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu		
500	505	510
Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg		
515	520	525
Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser		
530	535	540
Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu		
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Ala Glu Pro Gly Ser Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser		
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Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcacgc cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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ggggcagcct tccaccacgc ggagcccagc tgcagccgc ctcacaggaa 150  
gatgctgcgt cggcggggca gccctggcat ggggtgcat gtgggtgcag 200  
ccctgggagc actgtgttgc tgcctcacag gagccctgga ggtccaggtc 250  
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ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350  
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 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900  
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950  
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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09978295.101501

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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
	35	40	45
Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
	50	55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
	65	70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
	80	85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
	95	100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
	110	115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
	125	130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
	140	145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
	155	160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
	170	175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
	185	190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
	200	205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
	215	220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
	230	235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
	245	250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
	260	265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
	275	280	285
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	290	295	300

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 305 310 315

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<210> 138  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
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<210> 139  
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<220>  
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<400> 139  
 gctgtctgtc tgtctcattg 20

<210> 140  
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<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24  
 <212> DNA  
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<400> 141  
 tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
 <211> 24  
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<220>  
 <223> Synthetic oligonucleotide probe



<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150  
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200  
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
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 caactgggaa tataaccacga catgagacca gggtatagca caaattagca 1150  
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 145

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Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly	
				35					40					45	
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly	
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Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile	
				65					70					75	
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln	
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Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile	
				95					100					105	
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro	
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Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg	
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Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys	
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Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His	
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Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys	
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Leu

<210> 146  
<211> 26  
<212> DNA  
<213> Artificial Sequence



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<210> 150  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

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                   20                  25                  30  
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
                   35                  40                  45  
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
                   50                  55                  60  
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
                   65                  70                  75  
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
                   80                  85                  90  
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
                   95                  100                  105  
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu  
                   110                  115                  120  
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg  
                   125                  130                  135  
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu  
                   140                  145                  150  
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser  
                   155                  160                  165  
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val  
                   170                  175                  180  
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp  
                   185                  190                  195  
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro  
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 Asp Asp Gly Ala Lys  
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<210> 151

09978255.101501

<211> 524  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 103, 233  
<223> unknown base

<400> 151  
gttgtatatg tcctgaagta catccgtgca ttttttttag catccaacca 50  
tcctcccttg tagttctcgc cccctcaaat caccttctcc cttagcccac 100  
ccnactaaca tctcagtcctc tgaaaatgca cagagatgcc tggctacctc 150  
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ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
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aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
ctctgaggag atgttcctcc agttccgcat gaagatcatt aacctgaagc 400  
tggagcgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500  
caactgctac atcatgaacc cccc 524

<210> 152  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
tcacggggct catctctttt tctcttttgt gccaccagg acggagcatg 50  
gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100  
cctgccttgc accttcaact ccngctacac agtgaaccac aaacagttct 150  
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250  
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155  
cgctgacct gcacctcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156  
<211> 2680  
<212> DNA  
<213> Homo sapiens

<400> 156  
tgcggggacc gtcgtacacc atgggacctc acctccgccc ctaccgtgtg 50  
gggctgctcc cggatggcct cctgttctc ttgctgctgc taatgctgct 100  
cgcggaacca gcgctcccg cgggacgtca cccccagtg gtgctgggtcc 150  
ctggtgatatt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200  
gtgcactacc tctgtccaa gaagaccgaa agctaattca caatctggct 250  
gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300  
tcaggctggt ttacaacaaa acatccaggg ccacccagtt tcctgatggt 350  
gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400  
ggaccccgag aaaagcagcg tgggttcta tttccacacc atggtggaga 450  
gccttggtggg ctgggggtac acacggggtg aggatgtccg aggggctccc 500



tatgactggc gccgagcccc aatgaaaac gggccctact tcttggccct 550  
 ccgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggtgc 600  
 tggttgccca cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650  
 cagccgcagg cctggaagga caagtatatc cgggccttcg tgtcactggg 700  
 tgccgccttg gggggcgtag ccaagaccct gcgcgtcctg gcttcaggag 750  
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 actaccgcaa gttcttccag gacatcggct ttgaagatgg ctggctcatg 950  
 cggcaggaca cagaagggtt ggtggaagcc acgatgccac ctggcgtagc 1000  
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 ggtactgtga acttgaagag tgccctgcag tgccaggcct ggcagagccg 1150  
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 aagtgtgtt tggtatcctt tctctgtggc agtgaagaag gaagaaatga 1450  
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ccccagtc cgcaggctgt gttccagggg ccctgatttc ctcggatgtg 2000  
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ccaaggatga gagcaggggt tggagccatg gccttctggtg aacctatgga 2100  
gaaaggggaat ccaaggaagc agccaaggct gctcgcagct tccctgagct 2150  
gcacctcttg ctaacccccc catcacactg ccaccctgcc ctaggggtctc 2200  
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tggggctctg agcaggctgt atctggattc tggcaataaa agtactctgg 2650  
atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157  
<211> 412  
<212> PRT  
<213> Artificial

<400> 157  
Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp  
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Gly Leu Leu Phe Leu Leu Leu Leu Leu Met Leu Leu Ala Asp Pro  
20 25 30  
Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
35 40 45  
Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
50 55 60  
Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
65 70 75  
Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
80 85 90  
Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
95 100 105  
Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

110	115	120
Thr Phe Ser Leu Glu Phe Leu Asp Pro Ser Lys Ser Ser Val Gly		
125	130	135
Ser Tyr Phe His Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr		
140	145	150
Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg		
155	160	165
Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met		
170	175	180
Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val		
185	190	195
Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg		
200	205	210
Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser		
215	220	225
Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu		
230	235	240
Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys		
245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu		
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr		
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln		
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu		
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys		
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu		
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp		
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln		
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser		
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu		
395	400	405

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacgggcc ctacttctg gccctccgag agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

cggacgcgtg ggcgacgcg tggggcggcg gcagcggcgg cgacggcgac 50

atggagagcg gggcctacgg cgcgccaag gcggcggt ccttcgacct 100

gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcctgcatct atggtgaggg ctacagcaat 200

gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgcgcgtat ggcagtgcc tgggggtgct ggccttctg gcctcgacct 300

tcttcttggg ggtcgacgcg ttttcccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
 acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500  
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 cctgtgcca gagggcttca gtcagccgt cactcctcca gggcactttt 950  
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 gcgttctctg ccaaagactc gtgggggcca tcacacctgc cctgtgcagc 1150  
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 tgctcccacc cctggcagca gggaagggt ttgctgaca acaccagct 1350  
 ttatgtaaat attctgcagt tgttacttag gaagcctggg gagggcagg 1400  
 gtgccccatg gctccagac tctgtctgtg ccgagtgtat tataaatcg 1450  
 tgggggagat gcccggcctg ggatgctgtt tggagacgga ataatgttt 1500  
 tctcattcaa ag 1512

<210> 162  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe  
 1 5 10 15  
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala  
 20 25 30



05978295-101501

<400> 164  
gtgtactgag cggcggtag 20

<210> 165  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
ctgaaggaga tggctgccct cac 23

<210> 166  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
gagccaccta ccctgctccg aggccaggcc tgcagggcct catcggccag 50  
agggtgatca gtgagcagaa ggatgccgt ggccgaggcc ccccagggtg 100  
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200  
cctggtgccc ctgtttgtgc tgcgtggcct gctcgtgctg gcttcggcgg 250  
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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

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ggtgagtggc catggcagg cagcctccag gttcggggtc gacacatctg 1850



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 aaggtgtggc agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000  
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<210> 169  
 <211> 802  
 <212> PRT  
 <213> Homo sapiens  
 <400> 169

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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

290										295					300				
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val					
				305					310					315					
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu					
				320					325					330					
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro					
				335					340					345					
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His					
				350					355					360					
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp					
				365					370					375					
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln					
				380					385					390					
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile					
				395					400					405					
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly					
				410					415					420					
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
				425					430					435					
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
				440					445					450					
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
				470					475					480					
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
				485					490					495					
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
				500					505					510					
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe					
				515					520					525					
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
				530					535					540					
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu					
				545					550					555					
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly					
				560					565					570					
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu					
				575					580					585					

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp  
590 595 600

Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met  
605 610 615

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln  
620 625 630

Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu  
635 640 645

Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val  
650 655 660

Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val  
665 670 675

Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly  
680 685 690

Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly  
695 700 705

Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro  
710 715 720

Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg  
725 730 735

Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln  
740 745 750

Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg  
755 760 765

Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg  
770 775 780

Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser  
785 790 795

Trp Ile Gln Gln Val Val Thr  
800

<210> 170  
<211> 1327  
<212> DNA  
<213> Homo sapiens

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gcacccaggg ccagtgagacg atccagaaca ggaggctgtg tggcttgccg 50  
atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100  
caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150  
tgcaactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctccgatgag 500  
 gagcactgtg actgtggcct ccaggggccc tccagccgca ttgttggtgg 550  
 agctgtgtcc tccgagggtg agtggccatg gcaggccagc ctccaggttc 600  
 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650  
 acagctgccc actgcttcca ggaggacagc atggcctcca cggtgctgtg 700  
 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgcgtgg cctggagagg 750  
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800  
 agccatgact acgacgtggc gctgctgcag ctgcaccacc cggtggtgcg 850  
 ctgcggccgc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900  
 agcccgccct gcaactgtgg attacgggct ggggcgcctt gcgcgagggc 950  
 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000  
 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcagtctgt 1050  
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100  
 ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150  
 ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200  
 ccgcacacac aggtgtgacg agctggatcc agcaagtggg gacctgagga 1250  
 actgcccccc tgcaaagcag ggcccaactc ctggactcag agagcccagg 1300  
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgctc cagg 24

<210> 172

<211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 172  
 taatccagca gtgcaggccg gg 22

<210> 173  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 173  
 atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 174  
 tgcctatgca ctgaggaggc agaag 25

<210> 175  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 175  
 aggcagggac acagagtcca ttcac 25

<210> 176  
 <211> 50  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 176  
 agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177  
 <211> 1510  
 <212> DNA  
 <213> Homo sapiens

<400> 177

ggacgagggc agatctcgtt ctggggcaag ccgttgacac tcgctccctg 50  
ccaccgcccc ggctccgtgc cgccaagttt tcattttcca ccttctctgc 100  
ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150  
gctggaaaca ccaagaggtg gtttttggtt tttaaaactt ctgtttcttg 200  
ggaggggggtg tggcggggca ggatgagcaa ctccgttctt ctgctctgtt 250  
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ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350  
tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400  
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450  
tgcagtttca acatgacagc taaaaccttt ttcattcattc acggatggac 500  
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550  
acacaagaga gaaagacgcc aatgtagttg tgggtgactg gctccccctg 600  
gcccaccagc tttacacgga tgcggtcaat aataccaggg tgggtgggaca 650  
cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700  
tcgggaatgt ccaattgatc ggctacagcc tcggagcgca cgtggccggg 750  
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cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900  
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caatgggggt gacttcagc caggctgtgg actcaacgat gtcttgggat 1000  
caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050  
gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100  
tgccttcag tgcaactgact ccaatcgctt caaaaagggg atctgtctga 1150  
gctgccgcaa gaaccgttgt aatagcattg gctacaatgc caagaaaatg 1200  
aggaacaaga ggaacagcaa aatgtacctt aaaacccggg caggcatgcc 1250  
tttcagaggt aaccttcagt ccctggagt tccctgagga aggcccttaa 1300  
tacctccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350  
agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400  
tgcatgtcct aggaaaggga atctttacaa aataaacagt gtggaccctt 1450





Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn  
245 250 255

Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val  
260 265 270

Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu  
275 280 285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser  
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg  
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg  
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg  
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro  
350

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240  
 <212> DNA  
 <213> Homo sapiens

<400> 182  
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 acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150  
 cggcaaagtt tggcccgaag aggaagtggc ctcaaaccgc ggcaggtggc 200  
 gaccaggcca gaccaggggc gctcgcctgc tgcgggcggg ctgtaggcga 250  
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 ctggggccag agcaccatg ggccagggt tcctgtctc ctacagccaa 950  
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atgaactcag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200  
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 ggtctggaca ctccatcctt gccaaacctc taccocaaaag tggccttaag 3050  
 caccggaatg ccaattaact agagacctc cagcccccaa ggggaggatt 3100  
 tgggcagaac ctgaggtttt gccatccaca atccotccta cagggcctgg 3150  
 ctcacaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200  
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183  
 <211> 713  
 <212> PRT  
 <213> Homo sapiens

<400> 183  
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Gly Gly Ala Leu  
 1 5 10 15  
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp  
 20 25 30  
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro  
 35 40 45  
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu  
 50 55 60  
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys  
 65 70 75  
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro  
 80 85 90  
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu  
 95 100 105  
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
 110 115 120  
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
 125 130 135  
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
 140 145 150  
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
 155 160 165  
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

170	175	180
Gly Leu Thr Pro Arg	Pro Val Pro Ser Leu Pro Cys Asn Val Thr	
185	190	195
Leu Glu Asp Phe Tyr	Gly Val Phe Ser Ser Pro Gly Tyr Thr His	
200	205	210
Leu Ala Ser Val Ser	His Pro Gln Ser Cys His Trp Leu Leu Asp	
215	220	225
Pro His Asp Gly Arg	Arg Leu Ala Val Arg Phe Thr Ala Leu Asp	
230	235	240
Leu Gly Phe Gly Asp	Ala Val His Val Tyr Asp Gly Pro Gly Pro	
245	250	255
Pro Glu Ser Ser Arg	Leu Leu Arg Ser Leu Thr His Phe Ser Asn	
260	265	270
Gly Lys Ala Val Thr	Val Glu Thr Leu Ser Gly Gln Ala Val Val	
275	280	285
Ser Tyr His Thr Val	Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala	
290	295	300
Thr Tyr His Val Arg	Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys	
305	310	315
Gly Leu Gly Ser Gly	Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg	
320	325	330
Cys Tyr Ser Glu Ala	Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala	
335	340	345
Asp Gly Thr Asp Glu	Glu Asp Cys Pro Gly Cys Pro Pro Gly His	
350	355	360
Phe Pro Cys Gly Ala	Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr	
365	370	375
Leu Pro Ala Asp Arg	Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly	
380	385	390
Ala Asp Glu Arg Arg	Cys Arg His Cys Gln Pro Gly Asn Phe Arg	
395	400	405
Cys Arg Asp Glu Lys	Cys Val Tyr Glu Thr Trp Val Cys Asp Gly	
410	415	420
Gln Pro Asp Cys Ala	Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr	
425	430	435
Val Leu Pro Arg Lys	Val Ile Thr Ala Ala Val Ile Gly Ser Leu	
440	445	450
Val Cys Gly Leu Leu	Leu Val Ile Ala Leu Gly Cys Thr Cys Lys	
455	460	465

Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro Leu	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgctgtgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
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gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100  
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccttctt gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgcggctggc actaactgtg acatctatga ccttttttat catgcacaa 250  
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
 atttttcata ctttttatatg tactcagact tgatcgatta atgaagtgg 350  
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450  
 agttgggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500  
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600  
 tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135
Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu
				140					145					150



Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgtatcg 50  
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgaccttttt tatnatcgca caagccccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcaactgg aacaacagta ttcatgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgtctg tgctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
cagccccgcg cgccggccga gtcgtgagc cgcggtgcc ggacgggacg 50  
ggaccggcta ggctggggcg gccccccggg ccccgccgtg ggcattgggcg 100  
cactggcccc ggctgtgctg ctgcctctgc tggcccagtg gctcctgcgc 150  
gccgcccccg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200  
cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggaccctg 250  
ccgagcgcca cgccgacggc ttggcgtcg ccctggagcc tgccctggcg 300  
tccccgcggg gcgcccga cttcttggcc atggtagaca acctgcaggg 350  
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400  
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450  
ggaacccgc actcctacat agacacgtac ttgacacag agaggtctag 500  
cacataccgc tccaagggtt ttgacgtcac agtgaagtac acacaaggaa 550  
gctggacggg cttcgttggg gaagacctg tcaccatccc caaaggcttc 600  
aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650  
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700  
cacttgccaa gccatcaagt tctctggaga ccttcttcga ctccctgggtg 750  
acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagccgg 800  
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 atgcgctggg gatcgggtgcc acggtgatgg agggcttcta cgtcatcttc 1350  
 gacagagccc agaagagggt gggcttcgca gcgagcccct gtgcagaaat 1400  
 tgcagggtgct gcagtgtctg aaatttccgg gcctttctca acagaggatg 1450  
 tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500  
 attgtgtcct atgcgctcat gaggctctgt ggagccatcc tccttgtctt 1550  
 aatcgtcctg ctgctgtctg cgttccgggtg tcagcgtcgc ccccgtagcc 1600  
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 caccgctctt caatctctgt tctgtctcca gatgccttct agattcactg 1800  
 tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850  
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196  
 <211> 518  
 <212> PRT  
 <213> Homo sapien

<400> 196  
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 1 5 10 15  
 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr  
 20 25 30  
 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
 35 40 45  
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
 50 55 60  
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala  
 65 70 75  
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg  
 80 85 90  
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu  
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	

395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp		
410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu		
425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr		
440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu		
455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly		
470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg		
485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser		
500	505	510
Ser Leu Val Arg His Arg Trp Lys		
515		

<210> 197  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 197  
 cgcagaagct acagattctc g 21

<210> 198  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 198  
 ggaaattgga ggccaaagc 19

<210> 199  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 ggatgtagcc agcaactgtg 20

09078295.101501  
TOSTOT"55282550

<210> 200  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttggtc gttctcttc 19

<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggtcctgtgc ctggatgg 18

<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttg tc 22

<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA

<213> Homo sapiens

<400> 205

cgcctccgcc ttccgaggct gacgcgcccg ggcgcggttc caggcctgtg 50  
cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100  
gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150  
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200  
ccccgccgtg cggcggcatg ggcaacctgc ggggcgcgac ggccgtggtc 250  
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300  
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 tctcggaat ttggatgtag tattttcagg cccaccctt attgattctg 1550  
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 cagggcaggg cagctggtat cgagggtgcc catgggagta aggggacgcc 1850  
 ttccgggcgg atgcagggtt ggggtcatct gtatctgaag cccctcgga 1900  
 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr  
 1 5 10 15  
 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly  
 20 25 30  
 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn  
 35 40 45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
 50 55 60  
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
 65 70 75  
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile  
 80 85 90  
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
 95 100 105  
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
 110 115 120  
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
 125 130 135  
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
 140 145 150



His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	365	370	375
Leu	Ser																

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcattggcc ttggacttgg ccag 24

<210> 208  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 208  
acgccagtgg cctcaagctg gttg 24

<210> 209  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 209  
ctttctgagc tctgagccac ggttgacat cctcatccac aatgc 45

<210> 210  
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<212> DNA  
<213> Homo sapiens

<400> 210  
ggaggagaca gcctcctggg gggcaggggt tccctgcctc tgcctcct 50  
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acccccagga ccagctgttc cagggcctg gccctgccag gatgagctgc 150  
caagcctcag gccagccacc tcccaccatc cgctgggtgc tgaatgggca 200  
gccctgagc atggtgcccc cagaccacaca ccacctcctg cctgatggga 250  
cccttctgct gctacagccc cctgcccggg gacatgccca cgatggccag 300  
gccctgtcca cagacctggg tgtctacaca tgtgaggcca gcaaccggct 350  
tggcacggca gtcagcagag gcgctcggt gtctgtggt gtcctccggg 400  
aggatttcca gatccagcct cgggacatgg tggctgtggt gggtagcag 450  
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tgtccggggg gtccctgctg atggcaagag cagagaagag tgacgaagg 600  
acctacatgt gtgtggccac caacagcgca ggacatagg agagccgcgc 650  
agccccgggt tccatccagg agccccagga ctacacggag cctgtggagc 700  
ttctggctgt gcgaattcag ctggaaaatg tgacactgct gaaccggat 750

cctgcagagg gccccaagcc tagaccggcg gtgtgggtca gctggaaggt 800  
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tgtgtatcca ccgcccggcg cgagctaggg tgcacctggg ccaggtctg 1500  
tacagatata ccagttagga tgccatccta aaacacagga tggatcacag 1550  
tgactcccag tggttggcag acacttggcg ttccacctct ggctctoggg 1600  
acctgagcag cagcagcagc ctcagcagtc ggctgggggc ggatgcccgg 1650  
gacccactag actgtcgtcg ctccctgtc tcctgggact ccgaagccc 1700  
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ctcagacagc ctctgcagcc gcaggggact ctcttctccc cgcttgtctc 1900  
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gccaacagtt cccaotgct ccggggcagc cactccttgg agtcocgggc 2000  
ctgtgagtta ggaaatagag gttccaagaa cttttccaa agcccaggag 2050  
ctgtgcccc aactctggtt gcctggcggg ccctgggacc gaaactctc 2100  
agctcctcaa atgagotggt tactcgtcat ctccctccag caccctctt 2150  
tcctcatgaa actccccaa ctcagagtca acagaccag cctccggtgg 2200

caccacagge tccctectcc atcctgtgc cagcagcccc catccccatc 2250  
 cttagcccct gcagtcccc tagccccag gcctcttccc tctctggccc 2300  
 cagcccagct tccagtgcgc tgtccagctc ctactgtca tccctggggg 2350  
 aggatcaaga cagcgtgctg acccctgagg aggtagccct gtgcttgaa 2400  
 ctcaagtagg gtgaggagac tcccaggaac agcgtctctc ccatgccaa 2450  
 ggctccttca cccccacca cctatgggta catcagcgtc ccaacagcct 2500  
 cagagttcac ggacatgggc aggactggag gaggggtggg gcccaagggg 2550  
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 gggctcctta gccaatgggt ggggtcagc ctctgaggac aatgccgcca 2650  
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 tatgagaccg taggtcaaaa gcaccatcct cgtactgttg tcaactatgag 3650

ottaagaaat ttgataccat aaaatggtaa aaaaaaaaaa aaaaaaaaaa 3700

aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met Gly Gly Met Ala Gln Asp Ser Pro Pro Gln Ile Leu Val His  
1 5 10 15

Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser  
20 25 30

Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu  
35 40 45

Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu  
50 55 60

Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly  
65 70 75

His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr  
80 85 90

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly  
95 100 105

Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln  
110 115 120

Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu  
125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp  
140 145 150

Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val  
155 160 165

Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu  
170 175 180

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu  
185 190 195

Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr  
200 205 210

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val  
215 220 225

Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro  
230 235 240

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu <sup>4</sup> Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420
Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu			

530	535	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp 545	550	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser 560	565	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu 575	580	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp 590	595	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu 605	610	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln 620	625	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu 635	640	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser 650	655	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala 665	670	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg 680	685	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr 695	700	705
Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser 710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys 725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro 740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu 755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu 770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro 785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser 800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly 815	820	825

Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 212  
 gaagggacct acatgtgtgt ggcc 24

<210> 213  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 213  
 actgaccttc cagctgagcc acac 24

<210> 214  
 <211> 50  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

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ttgcctgctg ctcccaggtt atgaagccct ggaggggcca gaggaaatca 100  
gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150  
ctgaggggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200  
tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
agggcagggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300  
accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350  
cgaaaaacgg ggccccgatg agtctttact gatctctotg ttcgtctttc 400  
caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450  
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500  
attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550  
agacaggggc tgaggccct ccattgccag ggacttccca gtacgggcac 600  
gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650  
tcctgcaggg agtccccgcc ccccatgca gctggactcc acctcagcag 700  
aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750  
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agccctggag cccagagcgg tggccttgct cttccggctg gagactggga 1250  
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gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 216  
<211> 332  
<212> PRT  
<213> Homo sapiens

<400> 216  
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly  
1 5 10 15  
Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly  
20 25 30  
Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
35 40 45  
His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
50 55 60  
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met  
65 70 75  
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu  
80 85 90  
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr  
95 100 105  
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile  
110 115 120  
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser  
125 130 135  
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala  
140 145 150  
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu  
155 160 165  
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu  
170 175 180  
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr  
185 190 195  
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala		
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg		
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu		
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His		
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln		
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys		
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro		
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val		
320	325	330
Ser Ala		

- <210> 217
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 217
- ccctgcagtg cacctacagg gaag 24
- <210> 218
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 218
- ctgtcttccc ctgcttggt gtgg 24
- <210> 219
- <211> 47
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 219  
gggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtgga 100  
cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150  
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcaactcaagc 250  
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtggggc tccacctctg 350  
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gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgtacc 450  
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atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
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gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 221  
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser  
1 5 10 15  
Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
                   35                  40                  45  
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
                   50                  55                  60  
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
                   65                  70                  75  
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
                   80                  85                  90  
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
                   95                  100                  105  
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
                   110                  115                  120  
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
                   125                  130                  135  
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
                   140                  145

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 222  
 gggatcatgt tgttgccct ggtc 24

<210> 223  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 223  
 gcaaggcaga cccagtcagc cag 23

<210> 224  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 224  
 ctgcctgcta ccctccaagt gaggccaaagc tctacggtog ttgtg 45

<210> 225

<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccgggcccgg cgcccgcggc ggcacatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tctcgtctt cgccgtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaactgt cgtcgggtgg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctccgtgcgc cgcgggtgcc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgctctc ggcaagggtg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400  
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gacaggacag tgcattgggt cagccacag ggcttcact ggtcaggatg 500  
ctctgacaac atcgctacg gtgtggcctt ctccagtcg tttgtgatg 550  
tgccggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc caccgggtgt caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttcgc cagggtgggtc acgcaactga ggagaagttt 750  
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ctgggcacga ggggcgcac atgcaacaag acgtccaagg ccatcgacgg 950  
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ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccacctc cccaagaga tactggttgt attttttgtt 1200  
ctggttttgt ttttgggtcc tcatgttatt tattgccga accaggcagg 1250  
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ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350

gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400  
 acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
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 atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
 tacacatgga ctccctggcag cttgagccta gaagccatgt ctctcaaagt 1600  
 ccctgagaaa gggaacaagc agataccagg tcaagggcac cagggttcatt 1650  
 tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700  
 gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
 cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccg 1850  
 gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900  
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
 ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 226  
 Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
 1 5 10 15  
 Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
 20 25 30  
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
 35 40 45  
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
 50 55 60  
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
 65 70 75  
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
 80 85 90  
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
 95 100 105  
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
 110 115 120



Ala Phe Ala Val Thr Arg Ala Cys Ser	Ser Gly Glu Leu Glu Lys	125	130	135
Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe		140	145	150
Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe		155	160	165
Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser		170	175	180
Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg		185	190	195
Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly		200	205	210
Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro		215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		335	340	345
Glu Leu His Thr Cys Arg		350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 228  
 tggtagggaga ctgttttaaat tatcggcc 28

<210> 229  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 229  
 tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230  
 <211> 1355  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
 cggacgcgtg ggcggacgcg tggggcgacg cgtgggcgga cgcgtgggct 50  
 gggtagcctgc atcgccatgg acaccaccag gtacagcaag tggggcgga 100  
 gctccgagga ggtccccgga gggccctggg gacgctgggt gactggagc 150  
 aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200  
 ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250  
 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300  
 gcggcgctgg gtgcctgaa ggaggaggtc ggagactgcc acagctgctg 350  
 ctccgggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
 cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
 cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500  
 cactgagctg ttccggggcg tggaggccgt gaggtccag aacaactcct 550  
 gcgagccgtg cccacgctg tggtgtcct tcgagggctc ctgctacttt 600  
 ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650  
 tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggcttcc 700  
 tcaactcgaa cacgcgtggc cgtgggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
 cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
 agaactgtgt catgatgctg cacaoggggc tgtggaacga cgcaccgtgt 900  
 gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
 ccgcccagtg ccoctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000  
 gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050  
 tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100  
 tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcactcta 1150  
 actccactca cgcagaccca acctaactc cactagctcc aaaatccctg 1200  
 ctctgcgctc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250  
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
 aaaaa 1355

<210> 231  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 231  
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
     1                    5                    10                    15  
 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
                     20                    25                    30  
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
                     35                    40                    45  
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
                     50                    55                    60  
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
                     65                    70                    75  
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
                     80                    85                    90  
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
                     95                    100                    105  
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
                     110                    115                    120  
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
                     125                    130                    135



DO NOT WRITE IN THESE SPACES

<223> Synthetic oligonucleotide probe

caccgtgtga cagcqagaag gacggctgga tctgtgagaa aaggcacaac 50

<211> 1847

<213> Homo sapiens

gccaggggaa gagggatgac cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100

ctccacgctc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccggggag ccggcctcgg 200

gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgcgcg 350

gccagcctct tgggggagag tccatctggt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450

gtacccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccc 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700

cagcgcaggc actcgttggt ctctgtttgtg gtgcgcacatg tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca ctttctctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950

actacccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcata cctcccgccc cagtcctgcc 1050

cagcagggac aatgaqattg tagacagcgc ctcagttcca gaaacgccgc 1100

tggactgcga ggtctccctg tggctgctct ggggactgtg cggaggccac 1150  
 tgtgggaggg tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200  
 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250  
 tccctgataa ctgctgctaa gaccagagcc ccgcagcccc tggggccccc 1300  
 cggagccatg ggggtgtcggg ggctcctgtg caggtctatg ctgcaggcgg 1350  
 ccgagggcac aggggggtttc gcgctgctcc tgaccgcggt gagggccgcg 1400  
 cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450  
 aaacagcctc ctcccttccc aaccttgctt cttaggggcc cccgtgtccc 1500  
 gtctgtcttc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600  
 tgtccttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650  
 gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcccatcca 1700  
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
 1 5 10 15  
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
 20 25 30  
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
 35 40 45  
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
 50 55 60  
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
 65 70 75  
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
 80 85 90  
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
 95 100 105  
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val

110	115	120
His Glu Val Phe Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly Gln	
125	130	135
Thr Ser Ala Glu Leu Glu Val Gln Arg	Arg His Ser Leu Val Ser	
140	145	150
Phe Val Val Arg Ile Val Pro Ser Pro	Asp Trp Phe Val Gly Val	
155	160	165
Asp Ser Leu Asp Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala	
170	175	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe	
185	190	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val	
200	205	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe	
215	220	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr	
230	235	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala	
245	250	255
Pro Val Leu Pro Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser	
260	265	270
Val Pro Glu Thr Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser	
275	280	285
Trp Gly Leu Cys Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser	
290	295	300
Arg Thr Arg Tyr Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro	
305	310	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys	
320	325	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

097322/660  
105101 "5522/660

<210> 238  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 238  
caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagccccttc tctctctttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcaccgt gtctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tctctctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgctcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50  
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100  
aggaagagtgt tactcgtagg cggacagctt tagtggccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300  
cagaaatfff atccaactff gtttggaagc ttattatgac aataccattt 350  
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400  
acagggagtgt gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaattg 500  
ctggtttctca tgataatggc agccagtttt tcttcacact gggctcgagca 550  
gatgaactta acaataagca taccatcttt ggaaaggtta caggggatac 600  
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650  
gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaatcct 700  
tttcatgaca tcattccaag ggaattaaa aggctgaaaa aagagaaacc 750  
agaggaggaa gtaaagaaat tgaacccaa aggcacaaaa aatttttagtt 800  
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850  
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900  
ggatgatcca catctcagtt ctgttccagt ttagaaaagt gaaaaagggtg 950  
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000  
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050  
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100

aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250  
atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300  
aggaagcaac agtcaaagaa gggaacttcc cgggaagatc agacccttgc 1350  
actgctgaac cagttttaat ctaaactcac tcaagcaatt gctgaaacac 1400  
ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450  
tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500  
catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550  
ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650  
acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700  
gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750  
tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800  
catgtgtttt ttocctagctg acotttttata ttgctaaatc tgaaataaaa 1850  
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
<211> 472  
<212> PRT  
<213> Homo sapiens

<400> 245  
Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
1 5 10 15  
Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
20 25 30  
Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
35 40 45  
Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
50 55 60  
Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
65 70 75  
Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
80 85 90  
Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
95 100 105

Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala	110	115	120
Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly	125	130	135
Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu			

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met		
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp		
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg		
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met		
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249  
caactggaac aggaactgag atgtggatc 29

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
ctgggttcagc agtgcaaggg tctg 24

<210> 251  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 252  
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253  
<211> 2456  
<212> DNA  
<213> Homo sapiens

<400> 253  
cgccgccgtt ggggctggaa gttcccgcc ggtccgtgcc gggcgagaga 50  
gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtogagccct ggccagacat gtocacaggg 150  
ttctccttcg ggtccgggac totgggctcc accaccgtgg ccgccggcgg 200  
gaccagcaca ggccggcgttt tctccttcgg aacgggaacg tctagcaacc 250  
cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300  
actacatctg ctccttcaag tggttttgga accgggctct ttggatctaa 350  
acctgccact gggttcactc taggaggaac aaatacaggt gccttgaca 400

ccaagaggcc tcaagtggc accaaatatg gaaccctgca aggaaaacag 450  
atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500  
cagacctcct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550  
cctggaaagg aatcagagat gctaccacct acccgctgg atggagtctc 600  
gctctgtcgc caggctggag tgcagtggca cgatctcggc tcaactgcaac 650  
ctccgcctcc cgggttcaag cgagtctcct gcctcagcct ctgagtgtct 700  
ggggctacag gtgcctgcag gagtctggg gccagctggc ctgatgtac 750  
gtcagcacgc gggaacggta caagtggctg cgcttcagcg aggactgtct 800  
gtacctgaac gtgtacgcgc cggcgcgcg gcccgggat cccagctgc 850  
cagtgatggt ctggttcccg ggaggcgct tcatcgtgg cgctgcttct 900  
tcgtacgagg gctctgactt ggccgcccgc gagaaagtgg tgcgtgtgtt 950  
tctgcagcac aggctcggca tcttcggctt cctgagcacg gacgacagcc 1000  
acgcgcgcgg gaactggggg ctgctggacc agatggcggc totgcgctgg 1050  
gtgcaggaga acatcgcagc cttcggggga gaccagga atgtgaccct 1100  
gttcggccag tcggcggggg ccatgagcat ctgaggactg atgatgtcac 1150  
ccctagcctc gggctctctc catcggggcca tttccagag tggcaccgcg 1200  
ttattcagac ttttcatcac tagtaacca ctgaaagtgg ccaagaaggt 1250  
tgcccactg gctggatgca accacaacag cacacagatc ctggtaaact 1300  
gcctgagggc actatcaggg accaaggtga tgcgtgtgtc caacaagatg 1350  
agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400  
catgagccct gtggtgatg gtgtggtgat ccagatgac cctttggtgc 1450  
tcctgacca ggggaaggtt tcatctgtgc cctaccttct aggtgtcaac 1500  
aacctggaat tcaattggct cttgccttat aatatacca aggagcaggt 1550  
accacttggt gtggaggagt acctggacaa tgtcaatgag catgactgga 1600  
agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650  
tatgccacac tgcagactgc tcaactacc cagaaaaccc caatgatggg 1700  
aatctgccct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750  
ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800  
tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850

taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900  
caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950  
ccaccccagt ttagaactgc aggagctccc tgetgcctcc aggccaaagc 2000  
tagagctttt gctgtttgtg tgggacctgc actgcccttt ccagcctgac 2050  
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<210> 254  
<211> 545  
<212> PRT  
<213> Homo sapiens

<400> 254  
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35 40 45  
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
50 55 60  
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
65 70 75  
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
80 85 90  
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
95 100 105  
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
110 115 120  
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro			



425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu		
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn		
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp		
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met		
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr		
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala		
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu		
530	535	540
Pro Gln Glu Trp Ala		
545		

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

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<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

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 <212> DNA  
 <213> Homo sapiens

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 ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150  
 tgcattcttg tgccctgtct tttctctac ccccgacaag actggacagg 200  
 gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
 aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
 acccggggcc gattccagct cactggggat cccgccaagg ggaactgtct 350  
 cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttcttct 400  
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tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225
Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
				230					235					240
His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
				245					250					255

09073205-101501

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg		260	265	270
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro		275	280	285
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val		290	295	300
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly		305	310	315
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala		320	325	330
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln		335	340	345
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu		350	355	360
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser		365	370	375
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu		380	385	390
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile		395	400	405
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile		410	415	420
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe		425	430	435
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr		440	445	450
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn		455	460	465
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser		470	475	480
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu		485	490	495
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu		500	505	510
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg		515	520	525
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu		530	535	540
Val	Lys	Phe	Gln															

<210> 260  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 260  
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<210> 261  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 261  
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<210> 262  
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<220>  
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<400> 262  
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<210> 263  
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 <212> DNA  
 <213> Homo sapiens

<400> 263  
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 caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150  
 ttgagagtga agcgtggctg ggtgtggaac caatTTTTTg taccagagga 200  
 aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250  
 atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
 acttttatca ttgatgaaag aacaggtgac atatatgccca tacagaagct 350  
 tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
 tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
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<210> 264  
 <211> 772  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
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 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp  
 35 40 45  
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser  
 50 55 60



His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln				

350										355										360									
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr															
				365					370										375										
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly															
				380					385										390										
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg															
				395					400										405										
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly															
				410					415										420										
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp															
				425					430										435										
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln															
				440					445										450										
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp															
				455					460										465										
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu															
				470					475										480										
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp															
				485					490										495										
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser															
				500					505										510										
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln															
				515					520										525										
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu															
				530					535										540										
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn															
				545					550										555										
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val															
				560					565										570										
Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln															
				575					580										585										
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala															
				590					595										600										
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr															
				605					610										615										
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys															
				620					625										630										
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly															
				635					640										645										

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
755 760 765

Ser Ala Val Gln Ser Asn Asn  
770

<210> 265  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 24, 60, 141, 226, 228, 249, 252  
<223> unknown base

<400> 265  
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attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200  
aagaaagttt ataccgottg actgtntntg aatctgcacc cactgggant 250  
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcttgagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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 cccaaccccg acccagagct tctccagcgg cggcgcagcg agcagggctc 100  
 ccgccttaa cttctccgc ggggccagc caccttcggg agtccgggtt 150  
 gccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200  
 cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250  
 cattctcgcc ttcttgggat ggatcgccgc catcgtcagc actgccctgc 300  
 ccagtgag gatttactcc tatgcggcg acaacatcgt gaccgccag 350  
 gccatgtac aggggctgtg gatgtcctgc gtgtcgaga gcaccgggca 400  
 gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450  
 aagcaaccg tgccttgatg gtggttgga tctcctggg agtgatagca 500  
 atctttgtgg ccaccgttg catgaagtgt atgaagtgt tggaagacga 550  
 tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600

ttgcaggctct ggctatttta gttgccacag catggtatgg caatagaatc 650  
 gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700  
 tggtcaggct ctcttcaactg gctgggctgc tgcttctctc tgccttcttg 750  
 gaggtgcccct actttgctgt tccgtgcccc gaaaaacaac ctcttaccca 800  
 acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850  
 gtgacacaga ggcaaaagga gaaatcatg ttgaaacaaa ccgaaaatgg 900  
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950  
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000  
 gttaaaatac tcagtgttaa acatggctta atcttatttt atcttctttc 1050  
 ctcaatatag gagggaagat tttccattt gtattactgc tttccattga 1100  
 gtaatcatac tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150  
 tgtatatata catgtttttc tattaaaaat agacagtaaa atactattct 1200  
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250  
 atttaattcc atattgatga agatgtttat tggatatatt tctttttcgt 1300  
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 tttcaattct tcatgogtgc ccttttcata tacttatttt attttttacc 1450  
 ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500  
 tcattggtct ctatctoctg aatotaacac atttcatagc ctacatttta 1550  
 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600  
 tctttctgca tgaccaaagt gataaattcc tgttgacctt cccacacaat 1650  
 ccctgtactc tgacccatag cactottggt tgctttgaaa atatttgtcc 1700  
 aattgagtag ctgcatgctg tttccccagg tgttgtaaca caactttatt 1750  
 gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800  
 ctttttgttc cccattcctt aattgtattg ttttccaag tgtaattatc 1850  
 atgcgtttta tatcttcta ataagggtgtg gtctgtttgt ctgaacaaag 1900  
 tgctagactt tctggagtga taatctggtg acaaatattc tctctgtagc 1950  
 tgtaagcaag tcaactaatc tttctaccto ttttttctat ctgccaaatt 2000  
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050



Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125		135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile	Val Gln Glu Phe Tyr Asp	
140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr	Glu Phe Gly Gln Ala Leu	
155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys	Leu Leu Gly Gly Ala	
170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr		
185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr		
200	205	210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150  
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350  
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450  
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggtctctctt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttcctg tocc 564

<210> 272  
 <211> 498

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
<223> unknown base

<400> 272  
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50  
tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100  
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150  
acatcgtgac cggccaggcc ntgtacgagg ggctgtggat gtccctgcgtg 200  
tcgcagagca ccgggcagat ccagtgc aaa gtctttgact cccttgctga 250  
atctgagcag cacattgcaa gcaaccctgt ccttgatggt ggttggcatc 300  
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350  
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
gggggcgcga tatttcttct tgcaggtctg gctatttttag ttgccacagc 450  
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273  
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gatgaancgc gccatontca gactccctgc cccatggaga tttnnccat 100  
gctggcgaca acatcntgac ccccgacct gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac cntgcccotg atggtggttg 250  
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgggaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450



ccagtcacat gccaggtacg aatttggtca ggctctcttc actggctggg 500  
 ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttctgc 550  
 ga 552

<210> 274  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
 <223> unknown base

<400> 274  
 attctccct cctggatgga tgcncacc gtcacattgc cttccccan 50  
 tggaggattn actcctatgc tggcgacaac atcgtgaccc ccagggccat 100  
 ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
 ccagtcaaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
 caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
 ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300  
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350  
 caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400  
 cnnnnntct atgacctat gacccagtc aatgccaggt acgaatttgg 450  
 tcaggtcttc ttcactggtt gggctgctgc ttctctctgc cttctgggag 500  
 gtgccctact ttgctgttcc tgtccc 526

<210> 275  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
 <223> unknown base

<400> 275  
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 tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
 gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
 tgccaggtac gaatttggtc aggcctctctt cactggctgg gctgctgctt 350  
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
 <223> unknown base

<400> 276  
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 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggtt ggcattcttc 200  
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
 cgcgatattt cttnttgca gtcctgctat tttagttgcc acagcatggt 350  
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400  
 gccaggtacg aatttggtca ggcttnttc actggctggg ctgctgcttn 450  
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277  
 <211> 200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 34, 87, 138, 147, 163, 165-166, 172  
 <223> unknown base

<400> 277  
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 cccagtcaa tgccaggtac gaatttggtc aggcctctntt cactggntgg 150  
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200



ggggcgcgat atttcttctt gcaggtcttg ctattntag ttgccacagc 400  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
 tcaatgccag gtacgaattt ggtcaggctc tcttactgg ctgggctgct 500  
 gcttctctct gccttctggg aggtgcccta ctttctgtt cctgcgaa 548

<210> 280

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

cgagcgagtc atggccaacg c 21

<210> 281

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

gtgtcacacg tagtctttcc cgctgg 26

<210> 282

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggttcat tctcgcttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

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taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200

ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttea 300

ccgatgttgt caccaccaac cttaaagcttg gcaacccgac agaccgaaat 350  
 gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
 caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
 tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
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 attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700  
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 ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
 cccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
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 gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050  
 aattaatgta tgatgacac tcacaggtct tgcctttaaa ttaccctcc 1100  
 ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
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 ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250  
 aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
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 aagccatcag ctcttggga ctgatgaaca gagtcagaag cccaaaggaa 1500  
 ttgcactgtg gcagcatcag acgtactcgt cataagttag aggcgtgtgt 1550  
 tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttccact 1600  
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 ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatt 1700  
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ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800  
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 agagctgccca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900  
 gggagggaata ttctcagtag tgacagtcaa ctctaggtta ctttttttaa 1950  
 tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000  
 actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050  
 ggacctagcc tggagtcagg acaaatggat cgggctgcag aggggtagaa 2100  
 gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
 tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200  
 atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250  
 agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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				20					25					30
Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
				35					40					45
Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
				50					55					60
Ile	Asp	Ala	Gly	Ala	Ser	Ile	Asn	Val	Ser	Val	Met	Leu	Gln	Pro
				65					70					75
Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
				80					85					90
Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
				95					100					105
Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
				110					115					120
Cys	Val	Phe	Glu	Leu	Pro	Ala	Glu	Asn	Asp	Lys	Pro	His	Asp	Val
				125					130					135
Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
				140					145					150

Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu  
155 160 165

Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val  
170 175 180

Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly  
185 190 195

Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala  
200 205 210

Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu  
215 220 225

Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys  
230 235 240

Ile Ala Leu

<210> 285  
<211> 418  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 40, 53, 68, 119, 134, 177-178, 255  
<223> unknown base

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cagcagtttt ggggtggggag caagggnnga gagaaactct tcagcgaatc 200  
cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286  
<211> 543  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 73, 97

# SECRET

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gggagctgga gcccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgtctt 350  
gttcacttaa agggaaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
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gctgaactct gttgggtgaa ctgggtattgc tgctggaggg ctg 543

<213> Homo sapiens

<223> unknown base

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catatccatg ggattttaat ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaaat gtatagtaac 270
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<213> Homo sapiens

<223> unknown base



<400> 288  
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 gcaactgtggc agcatnagac gtacttgtna taagtgaagag gcgtgtgttg 150  
 actgattgac ccagcgcttt ggaaataaat ggcagtgtt tgttcantta 200  
 aagggaacaa gctaaatttg tatttggttca tgtagtgaag tcaaactgtt 250  
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400  
 ttggagagtc tggatcatgt gaggtggg 428

<210> 289  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
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 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
 tactcgtcat aagtgaagag cgtgtgttga ctgattgacc cagcgctttg 150  
 gaaataaatg gcagtgtttt gttcacttaa agggaccaag ctaaatttgt 200  
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
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 gtacagttaa tgctgcgtgc 320

<210> 290  
 <211> 609  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
 447, 481, 513, 532, 584, 598  
 <223> unknown base

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 gaaacntgn gtaatgccac aatggcatat tgtaaagtgc attttaaaca 100  
 ttggtaggcc ttggtacatg atgctggatt acctctctta aatgacacc 150  
 cttctctgcc tgttgggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
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 atgcatatth aanttattta atgtatttca tntcatgttt tcttattgtc 550  
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 gtattgctg 609

<210> 291  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
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 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
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 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
 gcgtgctgct gaactctgtt gggagaactg gtattgctgc tggagggctg 450  
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<210> 292  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 292  
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293  
 <211> 23  
 <212> DNA

# CONFIDENTIAL

<223> Synthetic oligonucleotide probe

aaccaccaga gccaaagagcc ggg 23

<211> 50

## <212> DNA

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

cagcggaaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<211> 2530

**<212> DNA**

<213> Homo sapiens

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

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gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagttca gtgccatgat catgqtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

at tt t t a t g t g g c a c t t g a g a a a g g t a c c c c g g a t t g t c a g t g a a a g g a c t 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccqactca 600

aaatatcacc acaaagggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttggaca aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg qcatttctcat 750

ttcccctcag catgttctaa ctgctgcccc ctgtgttcoat gatggaaagg 800

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cctagtttag aaataggga gctgagacat tttaagatct caagttttta 2250  
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cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 296

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				20					25					30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	
				35					40					45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	
				50					55					60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	
				65					70					75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	
				80					85					90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	
				95					100					105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	
				110					115					120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	
				125					130					135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	
				140					145					150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	
				155					160					165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	
				170					175					180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	
				185					190					195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	
				200					205					210	

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu  
215 220 225

Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln  
230 235 240

Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys  
245 250 255

Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp  
260 265 270

Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala  
275 280 285

His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys  
290 295 300

Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp  
305 310 315

Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu  
320 325 330

Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser  
335 340 345

Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys  
350 355 360

Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp  
365 370 375

Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg  
380 385 390

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly  
395 400 405

Asn Asp Ala Asn Cys Ala Tyr Gly  
410

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacatgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

# SECRET

<400> 298  
catcgttccc gtgaatccag aggc 24

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<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaagggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

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<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens
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<400> 300					
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tgtccgattc	tgattccggc	aaggatccaa	gcattggaatg	ctgccgtcgg	150
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tgccaaattg	ttggctgcga	tcaccagctg	ggaagcaccg	tcaaggaaga	650
taactgtggg	gtctgcaacg	gagatgggtc	cacctgccgg	ctgggtccgag	700
ggcagtataa	atcccagctc	tccgcaacca	aatcggatga	tactgtgggt	750
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cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950  
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 ttagtttcaa aaaaaaaaaa 1869

<210> 301  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<400> 301  
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 35 40 45  
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
 50 55 60





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365										370					375				
Pro	Leu	Pro	Arg	Trp	Glu	Ala	Thr	Pro	Trp	Thr	Ala	Cys	Ser	Ser					
380										385					390				
Ser	Cys	Gly	Gly	Gly	Ile	Gln	Ser	Arg	Ala	Val	Ser	Cys	Val	Glu					
395										400					405				
Glu	Asp	Ile	Gln	Gly	His	Val	Thr	Ser	Val	Glu	Glu	Trp	Lys	Cys					
410										415					420				
Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe					
425										430					435				
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440										445					450				
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp					
455										460					465				
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro					
470										475					480				
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro					
485										490					495				
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln					
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<210> 302
<211> 1533
<212> DNA
<213> Homo sapiens
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ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
tgctgatcac cggggcgaac agcggccttg gccgcgccac ggccgccgag 250
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 tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagtcca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatddd gatgacttga acagtgaaca aagctataat 700  
 aaaagctddd gttatagcog gagcaaaactg gctaacattc tttttaccag 750  
 ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900  
 agtagaaggt gccagactt ccatttattt ggcctcttca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatgggt ggcctgctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtatdddgg agttactgaa aaattatddd tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaatattd gtcagaatta agtgactcaa agtgctatcg 1400  
 agaggtdddd caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 303  
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
 1 5 10 15  
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
 20 25 30  
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
 35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala		50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg		65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu		80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly		95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg		110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg		125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr		140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His		155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys		170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr		185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser		200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile		215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val		230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly		245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu		260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr		275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly		290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala		305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val		320	325	330
Met	Val	Gly	Leu	Leu	Lys													

<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 34, 62, 87, 221, 229  
 <223> unknown base

<400> 304  
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
 gcaagaaaat tntgggatat cagtgaagtg atggtnngcc tgctaaaata 100  
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250  
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300  
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
 tggaaattat ctgcctggct t 521

<210> 305  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 305  
 ccaggaaatg ctccaggaag agcc 24

<210> 306  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 306  
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 307  
aacgcaggga tttccagtg cccttacatg aagactgaag atggg 45

<210> 308  
<211> 1523  
<212> DNA  
<213> Homo sapiens

<400> 308  
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100  
ccagcgcttg tcctgtcac ggacccagc gttaccatgc atcctgccgt 150  
cttctatcc ttaccgacc tcagatgctc ccttctgctc ctggttaact 200  
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250  
atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatatt gcgatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacct gccgattgtg acaaatttag 1050



Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

- <210> 310
- <211> 182
- <212> DNA
- <213> Homo sapiens
- <220>
- <221> unsure



<222> 36, 48  
 <223> unknown base

<400> 310  
 attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
 ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
 caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
 ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
 <211> 598  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
 <223> unknown base

<400> 311  
 agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
 gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggtcc 100  
 cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150  
 ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
 ctctctatcc ttaccgacc tcagatgctc ccttctgctc ctggttaactt 250  
 gggtttttac tctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
 atagatgaaa ttttaaana tgctgatgtg gctttagtca atttttatgc 350  
 tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
 ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
 agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
 caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
 aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 312  
 tgagaggcct ctctggaagt tg 22

<210> 313  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 313  
gtcagcgatc agtgaaagc 19

<210> 314  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 314  
ccagaatgaa gtagctcggc 20

<210> 315  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 315  
ccgactcaaa atgcattgtc 20

<210> 316  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 316  
catttggcag gaattgtcc 19

<210> 317  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 317  
ggtgctatag gccaaagg 18

<210> 318  
<211> 24  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctctt gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttctta tccttaaccg acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggagggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaaa 500

tgaagggtat ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600  
 ttttgcttgt ggaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgt ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcatctgtc atgtogatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt ctttaagcata agtaaactg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150  
 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200  
 ttctaacttg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
 1 5 10 15  
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30  
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45  
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60  
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75  
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90  
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120  
Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135  
Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323  
<211> 477  
<212> DNA  
<213> Homo sapiens

<400> 323  
attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
tgtaatacccc tgaatcccct tgtactccca gagtaccta tccacgcttt 100  
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
atatgcccct cttggcatat catatttga ggtatatgag tagaccagt 200  
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300  
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400  
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
gaatctgatc agttacttta aaaaatg 477

<210> 324  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 324  
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 325  
caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag ggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgetgacat ggccttgcc 150  
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
taoggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaate gaactaaatt 350  
ggaatgtgaa totgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450  
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
aactcttgct ctctcgggtga tggattgct ttggatttgt tgtgcaactg 850  
ttgctacagc tgtggagcag tatgttcct ctgagaagct gagtatctat 900  
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050  
ttttaaaaga caagtgaat agacatctaa aattocactc ctcatagagc 1100  
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
caaataaagt tactcaaate tgtg 1174

<210> 330  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 330  
Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly  
1 5 10 15  
Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser  
20 25 30  
Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr  
35 40 45  
Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr  
50 55 60  
Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg  
65 70 75  
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn  
80 85 90  
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser  
95 100 105  
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln  
110 115 120

Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met  
125 130 135

Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe  
140 145 150

Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser  
155 160 165

Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe  
170 175 180

Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu  
185 190 195

Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu  
200 205 210

Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly  
215 220 225

Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp  
230 235 240

Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp  
245 250 255

Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro  
260 265 270

Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu  
275 280 285

Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg  
290 295 300

Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys  
305 310 315

Val Asn Leu Ala His Ser Glu Ile  
320

<210> 331  
<211> 350  
<212> DNA  
<213> Homo sapiens

<400> 331  
ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccott 50  
gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100  
ggctgttttc aatttgtcag tttgtgatg atggaattga cttaaactga 150  
actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatttga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250



aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300

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<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

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aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100

cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150

tgctgaccat ggccttgcc ggaggttcgg ggaccgcttc ggctgaagca 200

tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250

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agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350

gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400

ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450

tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgcaaaa 500

atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550

gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
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<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
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agggcgacag gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggtctggga ttcttggttg 200  
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cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300  
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tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
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accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800  
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 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaatgtt 1200  
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 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
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 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
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 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
 20 25 30  
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
 35 40 45  
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
 50 55 60  
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
 65 70 75



365	370	375
Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp		
380	385	390
Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr		
395	400	405
Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu		
410	415	420
Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu		
425	430	435
Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile		
440	445	450
Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln		
455	460	465
Asn Ile His		

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
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 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttagaact tgtattttct ctacttaata gaactaaggg 350  
 ctttatccaa agtggtacca ttcttngagc gccagattt tcaactnttt 400  
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
 acttcatgaa atcaagtcac ttcttttgca ttttgatgag aattcatttt 500  
 tttgctg 507

<210> 339  
 <211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
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<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac tttcgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccaactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 343  
tgtccagaaa caggcacata tcagc 25

<210> 344  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

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gatgggaggg aaagtgaaga aaacagaaaa ggagaggac agaggccaga 100

ggacttctca tactggacag aaaccgatca ggcattggaac tccccctcgt 150

cactcacctg ttcttgcccc tgggtgttcct gacaggcttc tgcctcccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agagggtggt ggcagtgtct ctgaagggtc ataaaagaaa 550

aaagagaagt gtggaaggg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgtttctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800

attccagcct caggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900

gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950

gctacctaat gtgcttgcaa aagctccatg ttctctaaca gattcagact 1000

cctggccagg tgtggtggcc cacacctgta attctagcac ttggggaggc 1050

caagggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100

catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150

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 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
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 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 346  
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe  
 1 5 10 15  
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro  
 20 25 30  
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
 35 40 45  
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
 50 55 60  
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
 65 70 75  
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
 80 85 90  
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
 95 100 105  
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
 110 115 120  
 Phe Met Val Ser

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22  
 <223> unknown base

<400> 347



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 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
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 ggcattggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttcct 200  
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
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 ggggggtggac agcgatggat gctgggtggc gccccctggg atgggccttc 350  
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400  
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
 tggatgatgg 509

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

agggacagag gccagaggac ttc 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

caggtgcata ttcacagcag gatg 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

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<210> 351

<211> 2056

<212> DNA

<213> Homo sapiens

<400> 351

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gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
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tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
tctgctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
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aaaaaa 2056

<210> 352  
<211> 311  
<212> PRT  
<213> Homo sapiens

<400> 352  
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Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
20 25 30  
Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
35 40 45  
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
50 55 60  
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
65 70 75  
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
80 85 90  
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
95 100 105  
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser  
 125 130 135  
 Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe  
 140 145 150  
 His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe  
 155 160 165  
 Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val  
 170 175 180  
 Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met  
 185 190 195  
 Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
 200 205 210  
 Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
 215 220 225  
 Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 230 235 240  
 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp  
 245 250 255  
 Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val  
 260 265 270  
 Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
 275 280 285  
 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met  
 290 295 300  
 Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
 305 310

<210> 353  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748, 827  
 <223> unknown base

<400> 353  
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 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200



<400> 356  
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<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
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ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200  
tgagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250  
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aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450  
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aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gcccgtgga 800  
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gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300  
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 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
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<210> 358  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 358  
 Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu  
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 Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp  
 20 25 30  
 Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
 35 40 45  
 Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
 50 55 60  
 Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
 65 70 75  
 Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
 80 85 90  
 Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
 95 100 105  
 His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
 110 115 120  
 Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
 125 130 135  
 Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
 140 145 150  
 His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
 155 160 165  
 Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn		
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile		
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu		
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser		
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile		
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg		
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser		
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg		
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro		
305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg		
320	325	

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

ggcgcctggt tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50

ccgccagcct ccgccgccga gcctcggttcg tgtccccgcc cctcgctcct 100

gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag caccacgctc gcccccgac gctcggtgct caggcccttc 300

gcgagcgggg ctctocgtct gcggtccctt gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550

atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600

gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttgacc ttcataataa attacgaagt caggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850

ggcccccgac gtttcatgta caatcgtggt atgatgaagt gaaagacttt 900

agctacccat atgaacatga atgcaaccca tattgtccat tcaggtgttc 950

tggccctgta tgtacacatt atacacaggc cgtgtgggca actagtaaca 1000

gaatcgggtg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050

atatggccca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100

ctggtggggc catgcccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaaggg 1200  
tcagacaggt attatcccc tcgagaagag gaaacaaatg aaatagaacg 1250  
acagcagtc caagtccatg acacccatgt ccggacaaga tcagatgata 1300  
gtagcagaaa tgaagtcata agcgcacagc aaatgtccca aattgtttct 1350  
tgtgaagtaa gattaagaga tcagtgcata ggaacaacct gcaataggta 1400  
cgaatgtcct gctggctgtt tggatagtaa agctaaagtt attggcagtg 1450  
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggg 1500  
ataatagaca atgatgggtg ctgggtagat atcactagac aaggaagaaa 1550  
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaaatt 1600  
atcagtctgc taattccttc acagtctcta aagtaacagt tcaggctgtg 1650  
acttgtgaaa caactgtgga acagctctgt ccatttcata agcctgcttc 1700  
acattgcccc agagtatact gtcctcgtaa ctgtatgcaa gcaaatccac 1750  
attatgctcg tgtaattgga actcgagttt attctgatct gtccagtatc 1800  
tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtggttatgt 1850  
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900  
atggaatctt ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950  
agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000  
actattccaa atgcaatatt tctgaatttt gtataaaact gtaacattac 2050  
tgtacagagt acatcaacta ttttcagccc aaaaagggtgc caaatgcata 2100  
taaactctga taaacaaagt ctataaaata aaacatggga cattagcttt 2150  
gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaattatt 2200  
gctataatctt ctagcagtt atttctacag ttaattacat agtcatgatt 2250  
gttctacgtt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300  
tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgcatt 2350  
ttaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400  
agttcaatgc tatgccatta ccaactocaa ataactctca ataattttcc 2450  
acttaataac tgtaaagttt ttttctgtta atttaggcatt atagaatatt 2500  
aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550  
caaatgaatc tgttaaatg tttgattcct tgggaatggc cttaaaaata 2600

aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650  
 agtaaagtga ggggtaagca tggacagcca gagctttcta tgtactgtta 2700  
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctcctgcagg 2750  
 ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800  
 attaccattg ccaactgattt tttttaaatg gtaaatagacc ttgtatataa 2850  
 atattgccat atcatggtac ctataatggt gatataatttg tttctatgaa 2900  
 aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950  
 attttttttc tgctggtgga tttacatatt aaattttttc tgctggtgga 3000  
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 363  
 Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu  
 1 5 10 15  
 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr  
 20 25 30  
 Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu  
 35 40 45  
 Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn  
 50 55 60  
 Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln  
 65 70 75  
 Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val  
 80 85 90  
 Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp  
 95 100 105  
 Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu  
 110 115 120  
 Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln  
 125 130 135  
 Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His  
 140 145 150  
 Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys  
 155 160 165  
 Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

170					175					180				
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile
				185										195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly
				200										210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser
				215										225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys
				230										240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu
				245										255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His
				260										270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser
				275										285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg
				290										300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala
				305										315
Gly	Cys	Leu	Asp	Ser	Lys	Ala	Lys	Val	Ile	Gly	Ser	Val	His	Tyr
				320										330
Glu	Met	Gln	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly	Ile
				335										345
Ile	Asp	Asn	Asp	Gly	Gly	Trp	Val	Asp	Ile	Thr	Arg	Gln	Gly	Arg
				350										360
Lys	His	Tyr	Phe	Ile	Lys	Ser	Asn	Arg	Asn	Gly	Ile	Gln	Thr	Ile
				365										375
Gly	Lys	Tyr	Gln	Ser	Ala	Asn	Ser	Phe	Thr	Val	Ser	Lys	Val	Thr
				380										390
Val	Gln	Ala	Val	Thr	Cys	Glu	Thr	Thr	Val	Glu	Gln	Leu	Cys	Pro
				395										405
Phe	His	Lys	Pro	Ala	Ser	His	Cys	Pro	Arg	Val	Tyr	Cys	Pro	Arg
				410										420
Asn	Cys	Met	Gln	Ala	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Gly	Thr
				425										435
Arg	Val	Tyr	Ser	Asp	Leu	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Val	His
				440										450
Ala	Gly	Val	Val	Arg	Asn	His	Gly	Gly	Tyr	Val	Asp	Val	Met	Pro
				455										465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
485 490 495

Val Phe Ala Val Val  
500

<210> 364  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 364  
ggacagaatt tgggagcaca ctgg 24

<210> 365  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50  
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100  
agagaaagcc gagcagagct ggggtggcgtc tccgggcccgc cgctccgacg 150  
ggccagcggc ctccccatgt cctgtctccc acgccgcgcc cctccgggtca 200  
gcatgagget cctggcggcc gcgctgtctc tgetgtgtgt ggcgtgttac 250  
accgcgcgtg tggacgggtc caaatgcaag tgetcccga agggacccaa 300  
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350  
actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtac 400  
cgaggtcagg agcaactgcct gcaccccaag ctgcagagca ccaagcgctt 450  
catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500  
aggggtgaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550  
gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600  
aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650  
attgttatga agcaactttt accaacggtc agtttttaca ttttatagct 700  
gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgetccagac 750  
ttcatcacag gctgtttttt atcaaaaagg ggaaaactca tgcctttcct 800  
ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850  
ctttataagc gcccgaggagg aacaatgagc ttggtggaca catttcattg 900  
cagtgttgct ccattoctag cttgggaagc ttccgcttag aggtcctggc 950  
gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000  
ctcagtgtga ctccacagtg gcccotgtag ccgggcaagc aggagcaggt 1050  
ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100  
tgcttcattc cccctgggtt aatttttaca caccctagga aacatttcca 1150



<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccgggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

gccccaggga ctgctatggc ttcctttggt gttcaccccg gtctgcgtca 50  
 tggttaaactc caatgtcctc ctgtgggttaa ctgctcttgc catcaagttc 100  
 accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150  
 caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200  
 tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250  
 cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300  
 tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350  
 tgcatgacat gctgcccac tggtttaccg ccaatttgga tactttgatg 400  
 acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450  
 gccacaggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500  
 gtaatgaccg tggtaagac gaagatattc atgacagaa cagtaagaag 550  
 cccgtcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600  
 catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650



ccattaacta ccgtctggga atactagggt ttttaagta cggtgaccag 700  
 gcagcaaaag gcaactatgg gctcctggat cagattcaag cactgcggtg 750  
 gattgaggag aatgtgggag cctttggcgg ggaccccaag agagtgacca 800  
 tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850  
 cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900  
 cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950  
 tggcagacaa ggtcggtgc aacatgctgg acaccacgga catggtagaa 1000  
 tgcctgcgga acaagaacta caaggagctc atccagcaga ccatcacccc 1050  
 ggccacctac cacatagcct tggggccggt gatcgacggc gacgtcatcc 1100  
 cagacgaccc ccagatcctg atggagcaag gcgagttcct caactacgac 1150  
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 cgtggataac gaggacggtg tgacgcccaa cgactttgac ttctccgtgt 1250  
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 tacttctatg ccttctatca tcaactgcaa agcgaaatga agcccagctg 1500  
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 atgctcagcg ccgtggtcat gacctactgg acgaacttcg ccaaaactgg 1650  
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 aacgaaagtg gctttctggt tggaaactcg tcctcatttg cacaacttga 1850  
 acgagatatt ccagtatgtt tcaacaacca caaaggttcc tccaccagac 1900  
 atgacatcat ttccctatgg caccggcga tctcccgcca agatatggcc 1950  
 aaccaccaa cgcccagcaa tcaactctgc caacaatccc aaactctta 2000  
 aggacctca caaacaggg cctgaggaca caactgtcct cattgaaacc 2050  
 aaacgagatt attccaccga attaagtgtc accattgccg tcggggcgctc 2100

gctcctcttc ctcaacatct tagcttttgc ggcgctgtac tacaaaaagg 2150  
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 acaaatgata tcgctcacat ccagaacgaa gagatcatgt ctctgcagat 2250  
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 gacaaaacag tacaaattta ccccacggac attccaccac tagagtatag 2500  
 ctttgcctta tttcccttcc tatccctctg ccttaccgac tcagcaacat 2550  
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 aagatcaact tctgacctg tgaaatgtga gaagtacaca tttctgttaa 2750  
 aataactgct ttaagatctc taccactcca atcaatgttt agtgtgatag 2800  
 gacatcacca tttcaaggcc ccgggtgttt ccaacgtcat ggaagcagct 2850  
 gacacttctg aaactcagcc aaggacactt gatatttttt aattacaatg 2900  
 gaagttaa aa catttctttc tgtgccacac aatggatggc tctccttaag 2950  
 tgaagaaaga gtcaatgaga ttttcccag cacatggagc tgtaatccag 3000  
 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050  
 aatctgtacg gttctgtgca aagaggtggt ttgccagcct gaactatatt 3100  
 taagagactt tgt 3113

<210> 375  
 <211> 816  
 <212> PRT  
 <213> Homo sapiens

<400> 375  
 Met Leu Asn Ser Asn Val Leu Leu Trp Leu Thr Ala Leu Ala Ile  
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 Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn  
 20 25 30  
 Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn  
 35 40 45  
 Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala

50										55					60				
Ser	Pro	Pro	Thr	Gly 65	Glu	Arg	Arg	Phe	Gln 70	Pro	Pro	Glu	Pro	Pro 75					
Ser	Ser	Trp	Thr	Gly 80	Ile	Arg	Asn	Thr	Thr 85	Gln	Phe	Ala	Ala	Val 90					
Cys	Pro	Gln	His	Leu 95	Asp	Glu	Arg	Ser	Leu 100	Leu	His	Asp	Met	Leu 105					
Pro	Ile	Trp	Phe	Thr 110	Ala	Asn	Leu	Asp	Thr 115	Leu	Met	Thr	Tyr	Val 120					
Gln	Asp	Gln	Asn	Glu 125	Asp	Cys	Leu	Tyr	Leu 130	Asn	Ile	Tyr	Val	Pro 135					
Thr	Glu	Asp	Gly	Ala 140	Asn	Thr	Lys	Lys	Asn 145	Ala	Asp	Asp	Ile	Thr 150					
Ser	Asn	Asp	Arg	Gly 155	Glu	Asp	Glu	Asp	Ile 160	His	Asp	Gln	Asn	Ser 165					
Lys	Lys	Pro	Val	Met 170	Val	Tyr	Ile	His	Gly 175	Gly	Ser	Tyr	Met	Glu 180					
Gly	Thr	Gly	Asn	Met 185	Ile	Asp	Gly	Ser	Ile 190	Leu	Ala	Ser	Tyr	Gly 195					
Asn	Val	Ile	Val	Ile 200	Thr	Ile	Asn	Tyr	Arg 205	Leu	Gly	Ile	Leu	Gly 210					
Phe	Leu	Ser	Thr	Gly 215	Asp	Gln	Ala	Ala	Lys 220	Gly	Asn	Tyr	Gly	Leu 225					
Leu	Asp	Gln	Ile	Gln 230	Ala	Leu	Arg	Trp	Ile 235	Glu	Glu	Asn	Val	Gly 240					
Ala	Phe	Gly	Gly	Asp 245	Pro	Lys	Arg	Val	Thr 250	Ile	Phe	Gly	Ser	Gly 255					
Ala	Gly	Ala	Ser	Cys 260	Val	Ser	Leu	Leu	Thr 265	Leu	Ser	His	Tyr	Ser 270					
Glu	Gly	Leu	Phe	Gln 275	Lys	Ala	Ile	Ile	Gln 280	Ser	Gly	Thr	Ala	Leu 285					
Ser	Ser	Trp	Ala	Val 290	Asn	Tyr	Gln	Pro	Ala 295	Lys	Tyr	Thr	Arg	Ile 300					
Leu	Ala	Asp	Lys	Val 305	Gly	Cys	Asn	Met	Leu 310	Asp	Thr	Thr	Asp	Met 315					
Val	Glu	Cys	Leu	Arg 320	Asn	Lys	Asn	Tyr	Lys 325	Glu	Leu	Ile	Gln	Gln 330					
Thr	Ile	Thr	Pro	Ala 335	Thr	Tyr	His	Ile	Ala 340	Phe	Gly	Pro	Val	Ile 345					

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

[illegible]

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ttgttggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaactgt 150  
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ggccgcatg g 2461

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<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
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Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
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Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
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Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
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Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
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Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
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Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
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Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	



Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	275	280	285
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro	290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe	305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val	320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys	335	340	345
Arg Phe Tyr			

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<210> 382  
 <211> 24  
 <212> DNA  
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<220>  
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<400> 382  
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<210> 383  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<210> 384  
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 <212> DNA  
 <213> Homo sapiens

<400> 384

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 <211> 480  
 <212> PRT  
 <213> Homo sapiens

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 Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys  
 35 40 45  
 Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro  
 50 55 60  
 Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu  
 65 70 75  
 Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser  
 80 85 90  
 Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val  
 95 100 105  
 Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala  
 110 115 120  
 Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His  
 125 130 135  
 Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser  
 140 145 150  
 Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu  
 155 160 165  
 Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu  
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 Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr  
 200 205 210



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 <223> Synthetic oligonucleotide probe  
 <400> 386  
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<210> 387  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
 <400> 387  
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<210> 388  
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<210> 389  
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 <212> DNA  
 <213> Homo sapiens

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 aagccaccta ctgtctgcct atctatctat ctatctatct atctatctat 3000  
 ctatctatct atctatctat taotctcttg tacagacggg agtctcacgc 3050  
 ctgtaatccc agtacttttg gaggccgagg cgggtggatc acctgaggtt 3100  
 gggagtttga gaccagcctg accaaccatgg agaaacccc totatactaa 3150  
 aaaaatacaa aattagccgg gcgtgggtgt gcatgtctgt aatcccagct 3200  
 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggaggtt 3250  
 gcaatgagct gagattgtgc cattgcactc cagcctgggc aacaagagtg 3300  
 aaactctatc tca 3313

- <210> 390
- <211> 916
- <212> PRT
- <213> Homo sapiens
- <400> 390



Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu		1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln		20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val		35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala		50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe		65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile		80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn		95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu		110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu		125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met		140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn		155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu		170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val		185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu		200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr		215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro		230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu		245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp		260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp		275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr					

	290		295		300
Ile Ser Thr Ile	Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr			
	305	310			315
Gln Met Glu Val	Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg			
	320	325			330
Ala Lys Val Leu	Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro			
	335	340			345
Glu Val Val Leu	Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser			
	350	355			360
Pro Arg Gly Thr	Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp			
	365	370			375
Ser Glu Glu Asn	Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu			
	380	385			390
Pro Phe Lys Leu	Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val			
	395	400			405
Thr Asp Ile Val	Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile			
	410	415			420
Thr Val Thr Ala	Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu			
	425	430			435
Thr His Ile Ser	Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro			
	440	445			450
Val Phe Pro Gln	Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn			
	455	460			465
Pro Arg Gly Val	Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp			
	470	475			480
Cys Glu Glu Asn	Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr			
	485	490			495
Ile Gln Gly Ala	Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp			
	500	505			510
Thr Gly Val Leu	Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe			
	515	520			525
Arg Asp Leu Gln	Val Lys Val Met Ala	Arg Asp Asn Gly His Pro			
	530	535			540
Pro Leu Ser Ser	Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln			
	545	550			555
Asn Asp Asn Ala	Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp			
	560	565			570
Gly Ser Thr Gly	Val Glu Leu Ala Pro	Arg Ser Ala Glu Pro Gly			
	575	580			585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Lys	Arg	Asp	Ser	Gly	Gln
				590					595					600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly
				605					610					615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg
				620					625					630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala
				635					640					645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu
				650					655					660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu
				665					670					675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr
				680					685					690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu
				695					700					705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His
				710					715					720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala
				725					730					735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu
				740					745					750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys
				755					760					765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val
				770					775					780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly
				785					790					795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser
				800					805					810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser
				815					820					825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln
				830					835					840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn
				845					850					855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu

105101 56282660

875

880

885

Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
				905					910					915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggtccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg ccctggatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttctg ctcttgcctg ggggagcctg ggcaggacac tccagggcac 250  
aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300  
tggcaggcgg ccttgttcca gggccagcaa ctactctgtg gcggtgtcct 350  
tgtaggtggc aactgggtcc ttacagctgc ccactgtaa aaaccgaaat 400  
acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450  
caagaaatac ctgtgggtca gtccatccca caccctgtct acaacagcag 500  
cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550  
aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600  
accagcctg gccagaagtg caccgtctca ggetggggca ctgtcaccag 650  
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ttcccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750  
atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800  
tggaggcccc ctggtgtgtg atggtgcact ccagggcac acatcctggg 850  
gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900  
tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950  
ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	
				125					130					135	
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	
				140					145					150	
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	
				155					160					165	
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	
				170					175					180	
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	
				185					190					195	
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	
				200					205					210	
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	
				215					220					225	
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	
				230					235					240	
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	
				245					250					255	
Ile	Gly	Ser	Lys	Gly											
				260											

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

**SECRET**

<223> Synthetic oligonucleotide probe

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<211> 2236

<213> Homo sapiens

ggcgccgggtg	caccggggcgg	gctgagcgcc	tcctgcgggcc	cggcctgcgc	50
gccccggccc	gcgcgcgcgc	ccacgccccca	accccggccc	gcgcccccta	100
gccccgcgcc	gggcccgcgc	ccgcgcgccgc	gccaggtga	gcgtccgcc	150
cgccgcgagg	ccccgccccg	gcccgccccc	gccccgcccc	ggcggcgggg	200
ggaaccgggc	ggattcctcg	cgctcaaac	cacctgatcc	cataaaacat	250
tcctctccc	ggcgggccgc	gctgcgagcg	ccccgccagt	ccgcgcgcgc	300
gcgcacctcg	ccctgtgcgc	cctgcgcgcc	ctgcgcaccc	gcggcccag	350
cccagccaga	gccggggcga	gcggagcgcg	ccgagcctcg	tcccgcggcc	400
gggcgggggc	cgggccgtag	cggcggcgcc	tggatgcga	cccggccgcg	450
gggagacggg	cgcccgcgcc	gaaacgactt	tcagtccccg	acgcgccccg	500
cccaaccct	acgatgaaga	gggcgtccgc	tggaggagc	cggtgtctgg	550
catgggtgct	gtggctgcag	gcctggcagg	tggcagcccc	atgccaggt	600
gcctgcgtat	gctacaatga	gccaagggtg	acgacaagct	gccccagca	650
gggcctgcag	gctgtgcccg	tgggcatccc	tgctgccagc	cagcgcctct	700
tcctgcacgg	caaccgcctc	tcgcatgtgc	cagctgccag	cttcctgcc	750
tgccgcaacc	tcaccatcct	gtggctgcac	tcgaatgtgc	tggcccgaat	800
tgatggggct	gccttactg	gcctggccct	cctggagcag	ctggacctca	850
gcgataatgc	acagctcccg	tctgtggacc	ctgccacatt	ccacggcctg	900
ggccgcctac	acacgctgca	cctggaccgc	tgccgcctgc	aggagctggg	950
ccgggggctg	ttccgcggcc	tggctgccct	gcagtacctc	tacctgcagg	1000
acaacgcgct	gcaggcactg	cctgatgaca	ccttcgcga	cctgggcaac	1050
ctcacacacc	tcttctctgca	cggcaaccgc	atctccagcg	tgcccgagcg	1100

cgcttccgt gggctgcaca gctcgaccg tctcctactg caccagaacc 1150  
 gcgtggccca tgtgcaccog catgccttcc gtgaccttgg ccgcctcatg 1200  
 acactctatc tgtttgcaa caatctatca gcgctgcca ctgaggccct 1250  
 gggcccccctg cgtgccctgc agtacctgag gctcaacgac aaccctcggg 1300  
 tgtgtgactg ccggggcacgc ccactctggg cctgggtgca gaagttccgc 1350  
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400  
 tgacctcaaa cgcctagctg ccaatgacct gcagggctgc gctgtggcca 1450  
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 ctggggcttc ccaagtgtg ccagccagat gccgctgaca aggcctcagt 1550  
 actggagcct ggaagaccag cttcggcagg caatgcgctg aagggacgcg 1600  
 tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650  
 aatgactcac ctttggggac tctgcctggc tctgctgagc ccccgtcac 1700  
 tgagtgccg cccgagggct ccgagccacc aggggtcccc acctcgggcc 1750  
 ctgcgccgag gccaggtgtg tcacgcaaga accgcaccog cagccactgc 1800  
 cgtctggggc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850  
 ctcaggtgcc ctaccagcc tcacctgcag cctcaccccc ctgggccttg 1900  
 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950  
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000  
 ccgccaagcc agccggggcg ccgaccogtg gggcaggcca ggccaggtcc 2050  
 tccctgatgg acgcctgccg cccgccaccc ccatctccac cccatcatgt 2100  
 ttacaggggt cggcggcagc gtttgttcca gaacgcgcgc tcccaccag 2150  
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200  
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30



Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln	35	40	45
Gln Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln	50	55	60
Arg Ile Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala	65	70	75
Ser Phe Arg Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser	80	85	90
Asn Val Leu Ala Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala	95	100	105
Leu Leu Glu Gln Leu Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser	110	115	120
Val Asp Pro Ala Thr Phe His Gly Leu Gly Arg Leu His Thr Leu	125	130	135
His Leu Asp Arg Cys Gly Leu Gln Glu Leu Gly Pro Gly Leu Phe	140	145	150
Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr Leu Gln Asp Asn Ala	155	160	165
Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp Leu Gly Asn Leu	170	175	180
Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser Val Pro Glu	185	190	195
Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu Leu His	200	205	210
Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp Leu	215	220	225
Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala	230	235	240
Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu	245	250	255
Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro	260	265	270
Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val	275	280	285
Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg	290	295	300
Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro	305	310	315
Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu			

320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser		
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys		
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly		
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser		
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro		
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser		
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly		
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu		
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val		
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agcctcagat actgggggact ttacagtccc acagaaccgt cctcccagga 150  
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200  
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250  
cgcgggcgaa cctagaagct attctgtggt ggaggaaact gagggcagct 300  
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350  
tccaggcggg gggtaggggt tgtttccaga gggaacaaac tacatttgca 400  
gtcfaatcag gagaccgagg atttgttgct aaatgagaaa ttggaccgtg 450  
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500  
ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550  
aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600  
cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650  
ttagatgtag gccaaaacaa tattgagaac tatataatca gcccacactc 700  
ctattttcgg gtcctcaccg gcaaacgcag tgatggcagg aaatacccag 750  
agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800  
ttaacactca cagcactgga tggtaggtct cgcgccagat ctggcactgc 850  
tcagggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900  
agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950  
ctggttgtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000  
gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050  
agatcaatcc cttgacagga gaaattgaac taaaaaaaca actcgatttc 1100  
gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150



attttgtggc atttccatgc caatgtttat ttccccaat ttgtgtgtat 2650  
 gtaatatgtg acggatttac tcttgatttt tctcatgttc tttctccctt 2700  
 tgttttaag tgaacattta cctttattcc tgggtctt 2738

<210> 405  
 <211> 798  
 <212> PRT  
 <213> Homo sapiens

<400> 405  
 Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu  
 1 5 10 15  
 Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu  
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 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
 35 40 45  
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60  
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75  
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
 80 85 90  
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
 95 100 105  
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120  
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135  
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150  
 Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
 155 160 165  
 Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
 170 175 180  
 Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
 185 190 195  
 Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
 200 205 210  
 Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
 215 220 225  
 Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230										235					240				
Pro	Glu	Phe	Glu	Gln	Pro	Phe	Tyr	Arg	Val	Gln	Ile	Ser	Glu	Asp					
				245					250					255					
Ser	Pro	Val	Gly	Phe	Leu	Val	Val	Lys	Val	Ser	Ala	Thr	Asp	Val					
				260					265					270					
Asp	Thr	Gly	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Ser	Leu	Phe	Gln	Ala					
				275					280					285					
Ser	Glu	Glu	Ile	Gly	Lys	Thr	Phe	Lys	Ile	Asn	Pro	Leu	Thr	Gly					
				290					295					300					
Glu	Ile	Glu	Leu	Lys	Lys	Gln	Leu	Asp	Phe	Glu	Lys	Leu	Gln	Ser					
				305					310					315					
Tyr	Glu	Val	Asn	Ile	Glu	Ala	Arg	Asp	Ala	Gly	Thr	Phe	Ser	Gly					
				320					325					330					
Lys	Cys	Thr	Val	Leu	Ile	Gln	Val	Ile	Asp	Val	Asn	Asp	His	Ala					
				335					340					345					
Pro	Glu	Val	Thr	Met	Ser	Ala	Phe	Thr	Ser	Pro	Ile	Pro	Glu	Asn					
				350					355					360					
Ala	Pro	Glu	Thr	Val	Val	Ala	Leu	Phe	Ser	Val	Ser	Asp	Leu	Asp					
				365					370					375					
Ser	Gly	Glu	Asn	Gly	Lys	Ile	Ser	Cys	Ser	Ile	Gln	Glu	Asp	Leu					
				380					385					390					
Pro	Phe	Leu	Leu	Lys	Ser	Ala	Glu	Asn	Phe	Tyr	Thr	Leu	Leu	Thr					
				395					400					405					
Glu	Arg	Pro	Leu	Asp	Arg	Glu	Ser	Arg	Ala	Glu	Tyr	Asn	Ile	Thr					
				410					415					420					
Ile	Thr	Val	Thr	Asp	Leu	Gly	Thr	Pro	Met	Leu	Ile	Thr	Gln	Leu					
				425					430					435					
Asn	Met	Thr	Val	Leu	Ile	Ala	Asp	Val	Asn	Asp	Asn	Ala	Pro	Ala					
				440					445					450					
Phe	Thr	Gln	Thr	Ser	Tyr	Thr	Leu	Phe	Val	Arg	Glu	Asn	Asn	Ser					
				455					460					465					
Pro	Ala	Leu	His	Ile	Arg	Ser	Val	Ser	Ala	Thr	Asp	Arg	Asp	Ser					
				470					475					480					
Gly	Thr	Asn	Ala	Gln	Val	Thr	Tyr	Ser	Leu	Leu	Pro	Pro	Gln	Asp					
				485					490					495					
Pro	His	Leu	Pro	Leu	Thr	Ser	Leu	Val	Ser	Ile	Asn	Ala	Asp	Asn					
				500					505										

27.4

09978295.101501

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
				530					535					540	
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	
				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
				575					580					585	
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
				590					595					600	
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
				605					610					615	
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
				650					655					660	
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
				785					790					795	
Asn	Ile	Gln													

<210> 406

<211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 406  
 ctgagaacgc gcctgaaact gtg 23

<210> 407  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 407  
 agcgttgtca ttgacatcgg cg 22

<210> 408  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 408  
 ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
 <211> 1379  
 <212> DNA  
 <213> Homo sapiens

<400> 409  
 acccacgcgt ccgccacgc gtccgccac gcgtccgcc acgcgtccgc 50  
 gcgtagccgt gcgccgattg cctctcgcc tgggcaatgg tcccggctgc 100  
 cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150  
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
 agtggtcgt tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250  
 ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atgggccagg 300  
 acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350  
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500



cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600  
cccccagggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650  
actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700  
aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggcgccgct 750  
ttctgccag tttggcccct cactttaact ctctgccccg ggcatttcca 800  
gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850  
caggtttggc accgtagctg ttcctaataat tttattattt caaggagcta 900  
aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950  
atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000  
aactcaagcc gaccaaataag gccctcttcc cagcactttg ataaaaagtg 1050  
tggtactggtt gcttgatattt tccttattct ttttaattag ttttattatg 1100  
tatgctacca ttggaactga gagtattcgg tggctaattc caggacaaga 1150  
gcaggaacat gtggagtagt gatggctctga aagaagttgg aaagaggaac 1200  
ttcaatcctt cgtttcagaa attagtgcata cagtttcata cattttctcc 1250  
agtgcgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350  
caataagcaa atgcaaaaat attcaatag 1379

<210> 410  
<211> 360  
<212> PRT  
<213> Homo sapiens

<400> 410  
Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu  
1 5 10 15  
Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val  
20 25 30  
Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu  
35 40 45  
Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly  
50 55 60  
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala  
65 70 75  
Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80										85					90				
Met	Val	Met	Leu	Ser 95	Val	Ile	Pro	Gly	Glu 100	Ala	Glu	Asp	Lys	Val 105					
Ser	Ser	Glu	Pro	Ser 110	Gly	Val	Thr	Cys	Gly 115	Ala	Gly	Gly	Ala	Glu 120					
Asp	Ser	Arg	Cys	Asn 125	Val	Arg	Glu	Ser	Leu 130	Phe	Ser	Leu	Asp	Gly 135					
Ala	Gly	Ala	His	Phe 140	Pro	Asp	Arg	Glu	Glu 145	Glu	Tyr	Tyr	Thr	Glu 150					
Pro	Glu	Val	Ala	Glu 155	Ser	Asp	Ala	Ala	Pro 160	Thr	Glu	Asp	Ser	Asn 165					
Asn	Thr	Glu	Ser	Leu 170	Lys	Ser	Pro	Lys	Val 175	Asn	Cys	Glu	Glu	Arg 180					
Asn	Ile	Thr	Gly	Leu 185	Glu	Asn	Phe	Thr	Leu 190	Lys	Ile	Leu	Asn	Met 195					
Ser	Gln	Asp	Leu	Met 200	Asp	Phe	Leu	Asn	Pro 205	Asn	Gly	Ser	Asp	Cys 210					
Thr	Leu	Val	Leu	Phe 215	Tyr	Thr	Pro	Trp	Cys 220	Arg	Phe	Ser	Ala	Ser 225					
Leu	Ala	Pro	His	Phe 230	Asn	Ser	Leu	Pro	Arg 235	Ala	Phe	Pro	Ala	Leu 240					
His	Phe	Leu	Ala	Leu 245	Asp	Ala	Ser	Gln	His 250	Ser	Ser	Leu	Ser	Thr 255					
Arg	Phe	Gly	Thr	Val 260	Ala	Val	Pro	Asn	Ile 265	Leu	Leu	Phe	Gln	Gly 270					
Ala	Lys	Pro	Met	Ala 275	Arg	Phe	Asn	His	Thr 280	Asp	Arg	Thr	Leu	Glu 285					
Thr	Leu	Lys	Ile	Phe 290	Ile	Phe	Asn	Gln	Thr 295	Gly	Ile	Glu	Ala	Lys 300					
Lys	Asn	Val	Val	Val 305	Thr	Gln	Ala	Asp	Gln 310	Ile	Gly	Pro	Leu	Pro 315					
Ser	Thr	Leu	Ile	Lys 320	Ser	Val	Asp	Trp	Leu 325	Leu	Val	Phe	Ser	Leu 330					
Phe	Phe	Leu	Ile	Ser 335	Phe	Ile	Met	Tyr	Ala 340	Thr	Ile	Arg	Thr	Glu 345					
Ser	Ile	Arg	Trp	Leu 350	Ile	Pro	Gly	Gln	Glu 355	Gln	Glu	His	Val	Glu 360					

278

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 411  
cacagagcca gaagtggcgg aatc 24

<210> 412  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 412  
ccacatgttc ctgctcttgc cctgg 25

<210> 413  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 413  
cggtagtgc tgtactctag tcctgtttta caccctgtgg tgccg 45

<210> 414  
<211> 1196  
<212> DNA  
<213> Homo sapiens

<400> 414  
cccggctccg ctccctctgc cccctcgggg tcgcgcgccc acgatgctgc 50  
agggccctgg ctgcgtgctg ctgctcttcc tcgcctcgca ctgctgcctg 100  
ggctcggcgc gcgggctctt cctctttggc cagcccgact tctctacaa 150  
gcgcagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200  
togaatacca gaacatgcgg ctgccaacc tgctggggcca cgagaccatg 250  
aaggaggtgc tggagcaggc cggcgcttgg atcccgtgg tcatgaagca 300  
gtgccaccgc gacaccaaga agttcctgtg ctgcctcttc gcccccgtct 350  
gcctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400  
caggtgaagg accgctgcgc cccggtcatg tcgccttcg gcttcccctg 450  
gcccgacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500  
tcccctcgc tagcagcgc cacctcctgc cagccaccga ggaagctcca 550

aaggtatgtg aagcctgcaa aaataaaaat gatgatgaca acgacataat 600  
 ggaaacgctt tgtaaaaatg attttgcaact gaaaataaaa gtgaaggaga 650  
 taacctacat caaccgagat accaaaatca tcttgagac caagagcaag 700  
 accatttaca agctgaacgg tgtgtccgaa agggacctga agaatcggt 750  
 gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800  
 tcaacgcgcc ctatctggtc atgggacaga aacaggggtg ggagctgggtg 850  
 atcacctcgg tgaagcgggtg gcagaagggg cagagagagt tcaagcgcat 900  
 ctcccgacgc atccgcaagc tgcagtgcta gtcccgcat cctgatggct 950  
 ccgacaggcc tgctccagag cacggctgac catttctgct cgggatctc 1000  
 agctcccggt cccaagcac actcctagct gctccagtct cagcctgggc 1050  
 agcttcccc tgccttttgc acgtttgcat cccagcatt tctgagtta 1100  
 taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccaccc 1150  
 gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415  
 <211> 295  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Phe Leu Ala Ser  
 1 5 10 15  
 His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln  
 20 25 30  
 Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val  
 35 40 45  
 Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu  
 50 55 60  
 Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln  
 65 70 75  
 Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp  
 80 85 90  
 Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp  
 95 100 105  
 Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln  
 110 115 120  
 Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro  
 125 130 135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

cctggctcgc tgctgctgct c 21

<210> 417

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

cctcacaggt gcactgcaag ctgtc 25

<210> 418

<211> 47

<212> DNA

**SECRET**

<223> Synthetic oligonucleotide probe

ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<211> 1830

<213> Homo sapiens

gtggaggccg	ccgacgatgg	cggggccgac	ggaggccgag	acgggggttg	50
ccgagccccg	ggccctgtgc	gcgcagcggg	gccaccgcac	ctacgcgcgc	100
cgtctgggtgt	tcctgtctgc	gatcagcctg	ctcaactgct	ccaacgccac	150
gctgtggctc	agctttgcac	ctgtggctga	cgtcattgct	gaggacttg	200
tcctgtccat	ggagcagatc	aactggctgt	cactggctta	cctcgtggta	250
tccaccccat	ttggcgtggc	ggccatctgg	atcctggact	cogtcgggct	300
ccgtgcggcg	accatcctgg	gtgcgtggct	gaactttgcc	gggagtgtgc	350
tacgcatggt	gccctgcatg	gttgttgga	ccaaaaccc	atttgccttc	400
ctcatgggtg	gccagagcct	ctgtgccctt	gccagagcc	tggtcatctt	450
ctctocagcc	aagctggctg	ccttgtggtt	cccagagcac	cagcgagcca	500
cggccaacat	gctcgccacc	atgtcgaacc	ctctgggcgt	ccttgtggcc	550
aatgtgctgt	cccctgtgct	ggtcaagaag	ggtgaggaca	ttccgttaat	600
gctcgggtgc	tataccatcc	ctgctggcgt	cgtctgcctg	ctgtccacca	650
tctgcctgtg	ggagagtgtg	ccccccacc	cgccctctgc	cggggctgcc	700
agctccacct	cagagaagtt	cctggatggg	ctcaagctgc	agctcatgtg	750
gaacaaggcc	tatgtcatcc	tggtgtgtg	cttgggggga	atgatcggga	800
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cactccagtg	ggttttcogg	cctctgtggc	gctctcttca	tcacgttttg	900
gacctggggg	gcactggctc	tcggccccta	tgtggaccgg	accaagcact	950
tcactgaggc	caccaagatt	ggcctgtgcc	tgttctctct	ggcctgcgtg	1000
ccctttgccc	tggtgtccca	gctgcaggga	cagacccttg	coctggctgc	1050
cacctgctcg	ctgctcgggc	tgtttggctt	ctcggtgggc	cccgtagcca	1100

tggagttggc ggtcgagtgt tccttccccg tgggggaggg ggctgccaca 1150  
 ggcatgatct ttgtgctggg gcaggccgag ggaataactca tcatgctggc 1200  
 aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250  
 agcaggggga ggatccactt gactggacag tgtctctgct gctgatggcc 1300  
 ggctgtgca ccttcttcag ctgcatcctg gcggtcttct tccacacccc 1350  
 ataccggcgc ctgcaggccg agtctgggga gccccctcc acccgtaacg 1400  
 ccgtggggcg cgagactca gggccgggtg tggaccgagg gggagcagga 1450  
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 gggggcctcg ctagaggacc ccagagggcc cgggagcccc caccagcct 1550  
 gccaccgagc gactccccgt gcgcaaggcc cagcagccac cgacgcgccc 1600  
 tcccgccccg gcagactcgc aggcagggtc caagcgtcca ggtttattga 1650  
 cccggctggg tctcactcct ccttctcctc cccgtgggtg atcacgtagc 1700  
 tgagcgcctt gtagtccagg ttgcccgccca catcgatgga ggcgaactgg 1750  
 aacatctggt ccacctgcgg gcggggggcg aagggtcctc tgcgggctcc 1800  
 gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420  
 <211> 560  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
 Met Ala Gly Pro Thr Glu Ala Glu Thr Gly Leu Ala Glu Pro Arg  
 1 5 10 15  
 Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp  
 20 25 30  
 Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr  
 35 40 45  
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
 50 55 60  
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
 65 70 75  
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
 80 85 90  
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
 95 100 105  
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val

110										115					120				
Gly	Thr	Gln	Asn	Pro 125	Phe	Ala	Phe	Leu	Met 130	Gly	Gly	Gln	Ser	Leu 135					
Cys	Ala	Leu	Ala	Gln 140	Ser	Leu	Val	Ile	Phe 145	Ser	Pro	Ala	Lys	Leu 150					
Ala	Ala	Leu	Trp	Phe 155	Pro	Glu	His	Gln	Arg 160	Ala	Thr	Ala	Asn	Met 165					
Leu	Ala	Thr	Met	Ser 170	Asn	Pro	Leu	Gly	Val 175	Leu	Val	Ala	Asn	Val 180					
Leu	Ser	Pro	Val	Leu 185	Val	Lys	Lys	Gly	Glu 190	Asp	Ile	Pro	Leu	Met 195					
Leu	Gly	Val	Tyr	Thr 200	Ile	Pro	Ala	Gly	Val 205	Val	Cys	Leu	Leu	Ser 210					
Thr	Ile	Cys	Leu	Trp 215	Glu	Ser	Val	Pro	Pro 220	Thr	Pro	Pro	Ser	Ala 225					
Gly	Ala	Ala	Ser	Ser 230	Thr	Ser	Glu	Lys	Phe 235	Leu	Asp	Gly	Leu	Lys 240					
Leu	Gln	Leu	Met	Trp 245	Asn	Lys	Ala	Tyr	Val 250	Ile	Leu	Ala	Val	Cys 255					
Leu	Gly	Gly	Met	Ile 260	Gly	Ile	Ser	Ala	Ser 265	Phe	Ser	Ala	Leu	Leu 270					
Glu	Gln	Ile	Leu	Cys 275	Ala	Ser	Gly	His	Ser 280	Ser	Gly	Phe	Ser	Gly 285					
Leu	Cys	Gly	Ala	Leu 290	Phe	Ile	Thr	Phe	Gly 295	Ile	Leu	Gly	Ala	Leu 300					
Ala	Leu	Gly	Pro	Tyr 305	Val	Asp	Arg	Thr	Lys 310	His	Phe	Thr	Glu	Ala 315					
Thr	Lys	Ile	Gly	Leu 320	Cys	Leu	Phe	Ser	Leu 325	Ala	Cys	Val	Pro	Phe 330					
Ala	Leu	Val	Ser	Gln 335	Leu	Gln	Gly	Gln	Thr 340	Leu	Ala	Leu	Ala	Ala 345					
Thr	Cys	Ser	Leu	Leu 350	Gly	Leu	Phe	Gly	Phe 355	Ser	Val	Gly	Pro	Val 360					
Ala	Met	Glu	Leu	Ala 365	Val	Glu	Cys	Ser	Phe 370	Pro	Val	Gly	Glu	Gly 375					
Ala	Ala	Thr	Gly	Met 380	Ile	Phe	Val	Leu	Gly 385	Gln	Ala	Glu	Gly	Ile 390					
Leu	Ile	Met	Leu	Ala 395	Met	Thr	Ala	Leu	Thr 400	Val	Arg	Arg	Ser	Glu 405					



Pro	Ser	Leu	Ser	Thr	Cys	Gln	Gln	Gly	Glu	Asp	Pro	Leu	Asp	Trp	
				410					415					420	
Thr	Val	Ser	Leu	Leu	Leu	Met	Ala	Gly	Leu	Cys	Thr	Phe	Phe	Ser	
				425					430					435	
Cys	Ile	Leu	Ala	Val	Phe	Phe	His	Thr	Pro	Tyr	Arg	Arg	Leu	Gln	
				440					445					450	
Ala	Glu	Ser	Gly	Glu	Pro	Pro	Ser	Thr	Arg	Asn	Ala	Val	Gly	Gly	
				455					460					465	
Ala	Asp	Ser	Gly	Pro	Gly	Val	Asp	Arg	Gly	Gly	Ala	Gly	Arg	Ala	
				470					475					480	
Gly	Val	Leu	Gly	Pro	Ser	Thr	Ala	Thr	Pro	Glu	Cys	Thr	Ala	Arg	
				485					490					495	
Gly	Ala	Ser	Leu	Glu	Asp	Pro	Arg	Gly	Pro	Gly	Ser	Pro	His	Pro	
				500					505					510	
Ala	Cys	His	Arg	Ala	Thr	Pro	Arg	Ala	Gln	Gly	Pro	Ala	Ala	Thr	
				515					520					525	
Asp	Ala	Pro	Ser	Arg	Pro	Gly	Arg	Leu	Ala	Gly	Arg	Val	Gln	Ala	
				530					535					540	
Ser	Arg	Phe	Ile	Asp	Pro	Ala	Gly	Ser	His	Ser	Ser	Phe	Ser	Ser	
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Pro	Trp	Val	Ile	Thr											
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag ccctoctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cgggtcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150  
tggccttgcc ttggggctct gcttggttca taatcatcta actatgggac 200  
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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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Gly	Tyr	Leu	Phe	Leu	Leu	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	
				20					25					30	
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	
				35					40					45	
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	
				50					55					60	
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	
				65					70					75	
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	
				80					85					90	
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	
				95					100					105	
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	
				110					115					120	
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	
				125					130					135	
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	
				140					145					150	
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	
				155					160					165	
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	
				170					175					180	
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	
				185					190					195	

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
200		205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
215		220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
230		235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
245		250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
260		265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
275		280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
290		295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys	Asn
305		310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro	Asn
320		325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp	Val
335		340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln	Pro
350		355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala	Leu
365		370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val	His
380		385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg	Thr
395		400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp	Arg
410		415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp	Gln
425		430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln	Ile
440		445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg	Tyr
455		460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu	Ile
470		475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys	Val

485										490					495				
Ser	Tyr	Arg	Ile	Gln	Asp	Ser	Pro	Val	Ala	His	Leu	Val	Ala	Ile					
500										505					510				
Asp	Ser	Asn	Thr	Gly	Glu	Val	Thr	Ala	Gln	Arg	Ser	Leu	Asn	Tyr					
515										520					525				
Glu	Glu	Met	Ala	Gly	Phe	Glu	Phe	Gln	Val	Ile	Ala	Glu	Asp	Ser					
530										535					540				
Gly	Gln	Pro	Met	Leu	Ala	Ser	Ser	Val	Ser	Val	Trp	Val	Ser	Leu					
545										550					555				
Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Glu	Val	Val	Gln	Pro	Val	Leu					
560										565					570				
Ser	Asp	Gly	Lys	Ala	Ser	Leu	Ser	Val	Leu	Val	Asn	Ala	Ser	Thr					
575										580					585				
Gly	His	Leu	Leu	Val	Pro	Ile	Glu	Thr	Pro	Asn	Gly	Leu	Gly	Pro					
590										595					600				
Ala	Gly	Thr	Asp	Thr	Pro	Pro	Leu	Ala	Thr	His	Ser	Ser	Arg	Pro					
605										610					615				
Phe	Leu	Leu	Thr	Thr	Ile	Val	Ala	Arg	Asp	Ala	Asp	Ser	Gly	Ala					
620										625					630				
Asn	Gly	Glu	Pro	Leu	Tyr	Ser	Ile	Arg	Asn	Gly	Asn	Glu	Ala	His					
635										640					645				
Leu	Phe	Ile	Leu	Asn	Pro	His	Thr	Gly	Gln	Leu	Phe	Val	Asn	Val					
650										655					660				
Thr	Asn	Ala	Ser	Ser	Leu	Ile	Gly	Ser	Glu	Trp	Glu	Leu	Glu	Ile					
665										670					675				
Val	Val	Glu	Asp	Gln	Gly	Ser	Pro	Pro	Leu	Gln	Thr	Arg	Ala	Leu					
680										685					690				
Leu	Arg	Val	Met	Phe	Val	Thr	Ser	Val	Asp	His	Leu	Arg	Asp	Ser					
695										700					705				
Ala	Arg	Lys	Pro	Gly	Ala	Leu	Ser	Met	Ser	Met	Leu	Thr	Val	Ile					
710										715					720				
Cys	Leu	Ala	Val	Leu	Leu	Gly	Ile	Phe	Gly	Leu	Ile	Leu	Ala	Leu					
725										730					735				
Phe	Met	Ser	Ile	Cys	Arg	Thr	Glu	Lys	Lys	Asp	Asn	Arg	Ala	Tyr					
740										745					750				
Asn	Cys	Arg	Glu	Ala	Glu	Ser	Thr	Tyr	Arg	Gln	Gln	Pro	Lys	Arg					
755										760					765				
Pro	Gln	Lys	His	Ile	Gln	Lys	Ala	Asp	Ile	His	Leu	Val	Pro	Val					
770										775					780				

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr	815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro	860	865	870
Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala			



1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180

1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
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Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggaacacatt cagtattgat gccagacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037



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<211> 455  
<212> PRT  
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20 25 30  
Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser  
35 40 45  
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
50 55 60  
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
65 70 75  
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
80 85 90  
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
95 100 105  
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser	125	130	135
Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val	140	145	150
Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly	155	160	165
Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn	170	175	180
Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln	185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala	200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser	215	220	225
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly	230	235	240
Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu	245	250	255
Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala	260	265	270
Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr	275	280	285
Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys	290	295	300
Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys	305	310	315
Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu	320	325	330
Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe	335	340	345
Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu	350	355	360
Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser	365	370	375
Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr	380	385	390
Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu	395	400	405
Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn			

410

415

420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu  
425 430 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu  
440 445 450

Lys Gln Met Ala Pro  
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<210> 431

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 78, 81, 113, 157, 224, 297

<223> unknown base

<400> 431

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ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200

gagctcatca tctttgaaat cttnggagta ttgaatagca gctcccgta 250

ttttcactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttntca 300

tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350

cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400

tttccag 407

<210> 432

<211> 457

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434

<223> unknown base

<400> 432

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ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagtcatca tntttgaaat nttaggagta 250  
 ttgaatagca gctcccgta ttttactgg aaaatgaacc tgtgtgtaat 300  
 tctgctgac ctggttttca tgggtgcctt ttacattggc tattttattg 350  
 tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400  
 ttatggctga cctttatgta tttnttntgg aaantaggag atccctttcc 450  
 cattctc 457

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<400> 434  
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<210> 435  
 <211> 41  
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<210> 436  
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 <213> Homo sapiens

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 gggcctccgg gatttgctac ctttttggct ccctgctcgt ogaactgctc 100  
 ttctcacggg ctgtcgcctt caatctggac gtgatgggtg ccttgcgcaa 150  
 ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200



tccccgtgtg acgttcctga gccgtaacct ggaagaaccc aagcaccagg 1700  
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 gccatgttcc agctccagga aaatgtcaaa gacaagcttc gggccattgt 1800  
 agtgaccttg tctacagtc tccagacccc tcggctccgg cgacaggctc 1850  
 ctggccaggg gctgcctcca gtggccccc tctcaatgc ccaccagccc 1900  
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 caagatctgc cagagcaatc tgcagctggt ccacgcccgc ttctgtaccc 2000  
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 ggtcaccaac ctgccatcgg acccagccca gcccaggct gatggggatg 2150  
 atgcccatag agcccagctc ctggatcagc ttctgactc actgcactac 2200  
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 gtgtggtgtt cagctgccc cctacagct ttgaccgagc ggctgtgctg 2950  
 catgtctggg gccgtctctg gaacagcacc tttctggagg agtactcagc 3000  
 tgtgaagtcc ctggaagtga ttgtccgggc caacatcaca gtgaagtcct 3050  
 ccataaagaa cttgatgctc cgagatgcct ccacagtgat ccagtgatg 3100





80										85										90									
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg															
				95					100					105															
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu															
				110					115					120															
Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly															
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Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val															
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Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val															
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Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu															
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Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly															
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Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His															
				200					205					210															
Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr															
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Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His															
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Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp															
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Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe															
				275					280					285															
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile															
				290					295					300															
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu															
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Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val															
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Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala															
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Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr															
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Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu															
				365					370					375															

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala	380	385	390
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	395	400	405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	410	415	420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	425	430	435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	440	445	450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	455	460	465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	470	475	480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	485	490	495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	500	505	510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	515	520	525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu	530	535	540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	545	550	555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln	560	565	570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn	575	580	585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser	590	595	600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	605	610	615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln	620	625	630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	635	640	645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr	650	655	660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp			

097825 10501

665	670	675
Gly Thr Thr Ala Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	
680	685	690
Leu Glu Leu Met Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	
695	700	705
Gln Ala Asp Gly Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	
710	715	720
Leu Pro Asp Ser Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	
725	730	735
Ala Glu Lys Pro Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	
740	745	750
Glu Cys Glu Leu Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	
755	760	765
Phe Tyr Leu Ile Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	
770	775	780
Glu Leu Glu Val Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	
785	790	795
Leu His Pro Val Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	
800	805	810
Leu Ser Ile Ala Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	
815	820	825
Gly Val Val Arg Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	
830	835	840
Gly Ser Lys Val Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	
845	850	855
Ser Leu Arg Thr Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	
860	865	870
His Glu Ile Ala Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	
875	880	885
Glu Leu Glu Gly Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	
890	895	900
Pro Arg Pro Asn Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	
905	910	915
Arg Arg Arg Glu Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	
920	925	930
Arg Gln Glu Pro Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	
935	940	945
Lys Lys Lys Asn Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	
950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala  
 965 970 975  
 Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu  
 980 985 990  
 Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn  
 995 1000 1005  
 Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala  
 1010 1015 1020  
 Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val  
 1025 1030 1035  
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 1040 1045 1050  
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 Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro  
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 Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser  
 1100 1105 1110  
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 Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr  
 1130 1135 1140  
 Ala

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<213> Homo sapiens

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cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgagctg 200  
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gaataaatgg tgttgcatg tgtgctatag attttgagat ctccggagat 1300  
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aaaaaaaaaa aaaa 1964

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<211> 436  
<212> PRT  
<213> Homo sapiens

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Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu  
35 40 45  
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

				50						55					60
Phe	Arg	Asp	Glu	Val 65	Glu	Asp	Asp	Tyr	Phe 70	Arg	Thr	Trp	Ser	Pro 75	
Gly	Lys	Pro	Phe	Asp 80	Gln	Ala	Leu	Asp	Pro 85	Ala	Lys	Asp	Pro	Cys 90	
Leu	Lys	Met	Lys	Cys 95	Ser	Arg	His	Lys	Val 100	Cys	Ile	Ala	Gln	Asp 105	
Ser	Gln	Thr	Ala	Val 110	Cys	Ile	Ser	His	Arg 115	Arg	Leu	Thr	His	Arg 120	
Met	Lys	Glu	Ala	Gly 125	Val	Asp	His	Arg	Gln 130	Trp	Arg	Gly	Pro	Ile 135	
Leu	Ser	Thr	Cys	Lys 140	Gln	Cys	Pro	Val	Val 145	Tyr	Pro	Ser	Pro	Val 150	
Cys	Gly	Ser	Asp	Gly 155	His	Thr	Tyr	Ser	Phe 160	Gln	Cys	Lys	Leu	Glu 165	
Tyr	Gln	Ala	Cys	Val 170	Leu	Gly	Lys	Gln	Ile 175	Ser	Val	Lys	Cys	Glu 180	
Gly	His	Cys	Pro	Cys 185	Pro	Ser	Asp	Lys	Pro 190	Thr	Ser	Thr	Ser	Arg 195	
Asn	Val	Lys	Arg	Ala 200	Cys	Ser	Asp	Leu	Glu 205	Phe	Arg	Glu	Val	Ala 210	
Asn	Arg	Leu	Arg	Asp 215	Trp	Phe	Lys	Ala	Leu 220	His	Glu	Ser	Gly	Ser 225	
Gln	Asn	Lys	Lys	Thr 230	Lys	Thr	Leu	Leu	Arg 235	Pro	Glu	Arg	Ser	Arg 240	
Phe	Asp	Thr	Ser	Ile 245	Leu	Pro	Ile	Cys	Lys 250	Asp	Ser	Leu	Gly	Trp 255	
Met	Phe	Asn	Arg	Leu 260	Asp	Thr	Asn	Tyr	Asp 265	Leu	Leu	Leu	Asp	Gln 270	
Ser	Glu	Leu	Arg	Ser 275	Ile	Tyr	Leu	Asp	Lys 280	Asn	Glu	Gln	Cys	Thr 285	
Lys	Ala	Phe	Phe	Asn 290	Ser	Cys	Asp	Thr	Tyr 295	Lys	Asp	Ser	Leu	Ile 300	
Ser	Asn	Asn	Glu	Trp 305	Cys	Tyr	Cys	Phe	Gln 310	Arg	Gln	Gln	Asp	Pro 315	
Pro	Cys	Gln	Thr	Glu 320	Leu	Ser	Asn	Ile	Gln 325	Lys	Arg	Gln	Gly	Val 330	
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<400> 446

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 tcaagtacta gtaatttaac ttcatcatga atgaactata atttttaagt 2300  
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 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550  
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<210> 447  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 447  
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 Ala Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro  
 20 25 30  
 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys  
 35 40 45  
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile  
 50 55 60  
 Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His  
 65 70 75  
 Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys  
 80 85 90  
 Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met  
 95 100 105  
 Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu		
125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp		
140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser		
155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe		
170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val		
185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser		
200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg		
215	220	225
Lys Ser Arg Thr		

<210> 448  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 448  
 cccagcaggg ctgggcgaca aga 23

<210> 449  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 449  
 gtcttccagt ttcatatcca ata 23

<210> 450  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 450  
 ccagaaggag cacggggaag ggcagccaga tcttgtcgcc cat 43

<210> 451  
 <211> 859  
 <212> DNA  
 <213> Homo sapiens

<400> 451  
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 gccctgcccc gtgtgtcctg gatgctgctt tcctgectca ttctcctgtg 150  
 tcagggttcaa ggtgaagaaa ccagaaagga actgccctct ccacggatca 200  
 gctgtcccaa aggctccaag gcctatggct cccctgcta tgcttgttt 250  
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300  
 ctctggaaaa ctggtgtctg tgctcagtg ggctgaggga tccttcgtgt 350  
 cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400  
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
 ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550  
 ctgaagtga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600  
 gttcaaggac tagggcaggt ggaagtcag cagcctcagc ttggcgtgca 650  
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700  
 ttctcccaa actgccctac ctgactacct tgctcatgac ctcttcttt 750  
 ttctttttt ttcaccttca ttccaggctt ttctctgtct tccatgtctt 800  
 gagatctcag agaataataa taaaatggt actttataaa aaaaaaaaaa 850  
 aaaaaaaaaa 859

<210> 452  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 452  
 Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
 1 5 10 15  
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
 20 25 30  
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
 35 40 45  
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

50	55	60
Trp Met Asp Ala Asp	Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys	
65	70	75
Leu Val Ser Val Leu	Ser Gly Ala Glu Gly Ser Phe Val Ser Ser	
80	85	90
Leu Val Arg Ser Ile	Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly	
95	100	105
Leu His Asp Pro Thr	Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp	
110	115	120
Glu Trp Ser Ser Thr	Asp Val Met Asn Tyr Phe Ala Trp Glu Lys	
125	130	135
Asn Pro Ser Thr Ile	Leu Asn Pro Gly His Cys Gly Ser Leu Ser	
140	145	150
Arg Ser Thr Gly Phe	Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala	
155	160	165
Lys Leu Pro Tyr Val	Cys Lys Phe Lys Asp	
170	175	

<210> 453  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<400> 453  
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 tggggtgaga gcacagagga gtgggccggg accatgcggg ggacgcggct 100  
 ggcgtcctg gcgctggtgc tggtgcctg cggagagctg gcgccggccc 150  
 tgcgtgcta cgtctgtccg gagccacag gagtgtcgga ctgtgtcacc 200  
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
 ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300  
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccgcg 400  
 tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
 tccgactgta gattccccgc ccaccccatg ggcctatgc ggcccagccc 500  
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
 1 5 10 15  
 Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
 20 25 30  
 Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
 35 40 45  
 Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
 50 55 60  
 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
 65 70 75  
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
 80 85 90  
 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
 95 100 105  
 Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
 110 115 120  
 Leu Ser Leu Arg Leu  
 125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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 agccgaaccg gcacggtttc gtggggaccc aggtctgcaa agtgacggtc 100  
 attttctctt tctttctccc tcttgagtc ttctgagatg atggctctgg 150  
 gcgcagcggg agctaccogg gtctttgtcg cgatggtagc ggcggctctc 200  
 ggcggccacc ctctgctggg agtgagcgcc acctgaact cggttctcaa 250  
 ttccaacgt atcaagaacc tgccccacc gctgggcggc gctgcggggc 300  
 acccaggctc tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caactaccag ccgtaccctg gcgcagagga 400  
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
 acgcaggcgt gcaaatctgt ctgcctgca ggaagcgccg aaaacgctgc 500  
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaacatca 600



ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650  
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 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
 catttaaaaa aaaaaaaaa 1518

<210> 456  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 456  
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 20 25 30  
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
 35 40 45  
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
 50 55 60  
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
 65 70 75

Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu  
80 85 90

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp  
95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg  
110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn  
125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile  
140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu  
155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His  
170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys  
185 190 195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys  
200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg  
215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser  
245 250 255

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 457  
<211> 638  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
509, 556  
<223> unknown base

<400> 457  
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catttttttt tctttctcct tcnggagtc tntgagang atggttttgg 150  
gcgcagcggg agctaaccg gttttttgtn gcgatggtag cggcggtttt 200

cggcggccac cttntgctgg gaggtagcgc caccttgaat cggttttcaa 250  
 ttccaacgnt atcaagaacc tgccccacc gntgggcggc gctgcggggc 300  
 acccaggntt tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caattaccag ccgtacccgt gcgcagagga 400  
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
 angcgggcgt gcaaatntgt ntngcctgca ggaagcgccg aaaacgctgc 500  
 atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
 tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
 ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458

<211> 4040

<212> DNA

<213> Homo sapiens

<400> 458

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 ttctctcctg cagcgggtgc ttgggctcgg ccaggcgggg tccgccgcca 150  
 gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
 gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
 ttcacagatt aatatttttg gggacagatt tgtgatgctt gattcacctt 300  
 tgaagtaatg tagacagaag ttctcaaatt tgcattattac atcaactgga 350  
 accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400  
 agaatgggag tctggttaaa taaagatgac tatatcagag acttgaaaag 450  
 gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500  
 atcaggattt ttacagttaa ctgggagtgt ccaaaactgc aagcagtaga 550  
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 aaaccggaat aaccctaatg cacatggcga ttttttaaaa ataatagag 650  
 catatgaagt actcaaagat gaagatctac ggaaaaagta tgacaaatat 700  
 ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750  
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 cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950  
 ctgttaactg tggatgatgat agaagtcttt gccgaatgaa aggagtcaac 1000  
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 tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900  
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tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650  
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agaagggtct gcaaactttt tctgtaaagg gccggtttat aaatatttta 2850  
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aacgattctt agctcagagc catacaaaag taggctggat tcagtccatg 3000  
gaccatagat tgctgtcccc ctgcacggac ttataatgtt tcagggtggct 3050  
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aaagtccact ttcccttcac gttttttggc tgacctgaaa agaggtaact 3150  
tagtttttgg tcaactgttc tcttaaaaat gctatcccta accatatatt 3200  
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 ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950  
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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys	1	5	10	15
Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val	20	25	30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr	35	40	45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu	50	55	60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly	65	70	75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly				

200										205					210				
Met	Ala	Pro	Val	Lys	Tyr	His	Gly	Asp	Arg	Ser	Lys	Glu	Ser	Leu					
				215					220					225					
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu					
				230					235					240					
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala					
				245					250					255					
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys					
				260					265					270					
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu					
				275					280					285					
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn					
				290					295					300					
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg					
				305					310					315					
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn					
				320					325					330					
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu					
				335					340					345					
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala					
				350					355					360					
Pro	Asp	Ile	Cys	Ser	Asn	Leu	Tyr	Val	Phe	Gln	Pro	Ser	Leu	Ala					
				365					370					375					
Val	Phe	Lys	Gly	Gln	Gly	Thr	Lys	Glu	Tyr	Glu	Ile	His	His	Gly					
				380					385					390					
Lys	Lys	Ile	Leu	Tyr	Asp	Ile	Leu	Ala	Phe	Ala	Lys	Glu	Ser	Val					
				395					400					405					
Asn	Ser	His	Val	Thr	Thr	Leu	Gly	Pro	Gln	Asn	Phe	Pro	Ala	Asn					
				410					415					420					
Asp	Lys	Glu	Pro	Trp	Leu	Val	Asp	Phe	Phe	Ala	Pro	Trp	Cys	Pro					
				425					430					435					
Pro	Cys	Arg	Ala	Leu	Leu	Pro	Glu	Leu	Arg	Arg	Ala	Ser	Asn	Leu					
				440					445					450					
Leu	Tyr	Gly	Gln	Leu	Lys	Phe	Gly	Thr	Leu	Asp	Cys	Thr	Val	His					
				455					460					465					
Glu	Gly	Leu	Cys	Asn	Met	Tyr	Asn	Ile	Gln	Ala	Tyr	Pro	Thr	Thr					
				470					475					480					
Val	Val	Phe	Asn	Gln	Ser	Asn	Ile	His	Glu	Tyr	Glu	Gly	His	His					
				485					490					495					

Ser Ala Glu Gln Ile Leu Glu Phe Ile	Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr	Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met	Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met	Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn	Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln	Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys	Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg	Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln	Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu	Gln Gly Lys Asn His Trp	635	640	645
Val Ile Asp Phe Tyr Ala Pro Trp Cys	Gly Pro Cys Gln Asn Phe	650	655	660
Ala Pro Glu Phe Glu Leu Leu Ala Arg	Met Ile Lys Gly Lys Val	665	670	675
Lys Ala Gly Lys Val Asp Cys Gln Ala	Tyr Ala Gln Thr Cys Gln	680	685	690
Lys Ala Gly Ile Arg Ala Tyr Pro Thr	Val Lys Phe Tyr Phe Tyr	695	700	705
Glu Arg Ala Lys Arg Asn Phe Gln Glu	Glu Gln Ile Asn Thr Arg	710	715	720
Asp Ala Lys Ala Ile Ala Ala Leu Ile	Ser Glu Lys Leu Glu Thr	725	730	735
Leu Arg Asn Gln Gly Lys Arg Asn Lys	Asp Glu Leu	740	745	

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 460  
actccccag ctgttcacac tgcc 24

<210> 461  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 461  
gatcagccag ccaataccag cagc 24

<210> 462  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463  
<211> 1818  
<212> DNA  
<213> Homo sapiens

<400> 463  
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ggacagagca aagccatgaa catcatccta gaaatccttc tgctttctgat 100  
caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300  
agtgcgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgata 450  
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550  
aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600  
ttccttacct catccatat tgttcagca aatttgccgc tgttggcttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

aacctcatgt ctctgccag tttttgtgaa tactgggttc accaaaaatc 750  
 caagcacaaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800  
 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850  
 tatcaatata tttctgagac tacagaagtt tcttcctgaa cgcgccctcag 900  
 cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950  
 aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000  
 ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050  
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 caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150  
 gtagtttttc ataggtctgt ttttccttcc atgcctctta aaaacttctg 1200  
 tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250  
 catttaaagg tggacaaaag ctacctccct aaaagtaaat acaaagagaa 1300  
 cttattttaca cagggaaggt ttaagactgt tcaagtagca ttccaatctg 1350  
 tagccatgcc acagaatata aacaagaaca cagaatgagt gcacagctaa 1400  
 gagatcaagt ttcagcaggc agctttatct caacctggac atatttttaag 1450  
 attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500  
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttotgtat 1550  
 aactctgaag tccacaaaaa gtggaccctc tatatttctc ccctttttat 1600  
 agtcttataa gatacattat gaaaggtgac cgactctatt ttaaactctca 1650  
 gaatttttaag ttctagcccc atgataacct tttcttttgt aatttatgct 1700  
 ttcatatata cttgggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800  
 atggacccaa gagaagaa 1818

<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
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 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
 20 25 30

Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	155	160	165
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	170	175	180
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	185	190	195
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	200	205	210
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	215	220	225
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	230	235	240
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	245	250	255
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	260	265	270
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	275	280	285
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	290	295	300

<210> 465  
 <211> 1547  
 <212> DNA  
 <213> Homo sapiens

<400> 465

cgccggcgcc tgcgggccc aggtgagggg cgcgaggtga gggcgcgag 50  
gttcccagca ggatgcccc gctctgcagg aagctgaagt gagaggcccc 100  
gagagggccc agcccggccc gggcaggatg accaaggccc ggctgttccg 150  
gctgtggctg gtgctgggg cggtgttcat gatcctgctg atcatcgtgt 200  
actgggacag cgcaggcgcc gcgcacttct acttgacac gtccttctct 250  
aggccgcaca cggggcgccc gctgccacg cccgggccc acagggacag 300  
ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350  
gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400  
cctgcgcggg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450  
gcgcgacgcc cggcgacgcc cagaccaggg cggcgacgag gcggagcgga 500  
ggagcgtgct ggggggcttc tgcgccaact ccagcctggc cttccccacc 550  
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cgtggacgac cggcacgggg ccatctactg ctacgtgcc aaggtggcct 650  
gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700  
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caacgccagc gcgcacctga cctcaacaa gttctggcg cgctacggga 800  
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ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250  
gctgggagga ggactgggtc gccaaagatcc ccctggcctg gaggcagcag 1300  
ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350  
cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgcgtg 1400  
cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatttt 1450



Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp  
410

<210> 467  
<211> 1071  
<212> DNA  
<213> Homo sapiens

<400> 467  
tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50  
ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100  
acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200  
cgggggccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350  
cctggattgt gttgtcaaca acgctggcca ccaccaccc ccacagaggc 400

ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaaccta 450  
 ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500  
 tcaagggaat gtcacccaaca tctccagcct ggtgggggca atcgccagag 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagcttttg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccg ctaggtcggg gctgcggcag tgttcctggc 800  
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900  
 cccgatatcc cttctgatt tctctcattt ctacttgggg ccccttcct 950  
 aggactctcc caccctaaac tccaacctgt atcagatgca gcccccaagc 1000  
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 ccataaaaac gatttgcagc c 1071

<210> 468  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 468  
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 Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
                     20                    25                    30  
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
                     35                    40                    45  
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
                     50                    55                    60  
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
                     65                    70                    75  
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
                     80                    85                    90  
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
                     95                    100                    105  
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
                     110                    115                    120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn	125	130	135
Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln	140	145	150
Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr	155	160	165
Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn	170	175	180
Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu	185	190	195
Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met	200	205	210
Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly	215	220	225
Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly	230	235	240
Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys	245	250	255
Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser	260	265	270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
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 cctcacaacc tgctgtttct tottaccatt tccatottcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300  
 acttgacgct gtggatgtcc aacaagagga gcctgtotcc ctggggctac 350  
 agcatcaacc acgacccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgag ccgccgctc 500  
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550



gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650  
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470  
<211> 180  
<212> PRT  
<213> Homo sapiens

<400> 470  
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20 25 30  
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
35 40 45  
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
50 55 60  
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
65 70 75  
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
80 85 90  
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile  
95 100 105  
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg  
110 115 120  
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp  
125 130 135  
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg  
140 145 150  
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln  
155 160 165  
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe  
170 175 180

<210> 471  
<211> 2368  
<212> DNA  
<213> Homo sapiens

<400> 471  
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ctccccgcgc agaagcctcg ctcggcgcgc aacatggcgg gtgggcgcgtg 150  
 cggccccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200  
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctccaa ctggacgtcg gtgatggagg gcgagtggat 300  
 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350  
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450  
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 agcaaccctg cccagctgac acagaggtgg tggaagactc cttgaggcag 1150  
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 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350  
 agggaggcta atttcttt 2368

<210> 472  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
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 20 25 30  
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	170	175	180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	185	190	195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	200	205	210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	215	220	225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	230	235	240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	245	250	255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	260	265	270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	275	280	285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	290	295	300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	305	310	315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	320	325	330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	335	340	345
Asp Lys Gly Leu																	

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
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<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
ctctcctcat ccacaccagc agcc 24

<210> 475  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<400> 476  
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gccacatga ttgactcag agattctctt ttgtccacag acagtcattct 100  
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tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
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 agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700  
 tcattttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750  
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800  
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850  
 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900  
 aagaaattga agggagaggc tgtgatttct gtatttgcg acctacaggt 950  
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 cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050  
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 tgccaccatg ccaggctaatt ttttggtgtt tttttagag actgggtttt 1200  
 gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgcc 1250  
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 gcccgaagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350  
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 tcaacaatgc cattgaagtgc cacggtgtgt tgccacgatt tgacctcaa 1450  
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 caagtagctg ggattacagt caggcaccac cacacccggc taattttgta 1850  
 tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900  
 ctctgacct caagtgatct gcctgcctcg gcctcccaag tgctgggatt 1950  
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 gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050



	170		175		180
Val	Ile	Tyr	Asp	Gln	Leu
				Cys	Ser
				Val	Pro
				Ser	Tyr
				Ser	Ile
				Cys	
				185	190
					195
Glu	Lys	Lys	Phe	Ser	Met
				200	

<210> 478  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 478  
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<210> 479  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 479  
 acaagtgtct tcccaacctg 20

<210> 480  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 480  
 atcctcccag agccatggta cctc 24

<210> 481  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 481  
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<210> 482  
 <211> 3819  
 <212> DNA  
 <213> Homo sapiens



<400> 482

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<210> 483  
 <211> 693  
 <212> PRT  
 <213> Homo. sapiens

<400> 483  
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 20 25 30  
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
 35 40 45  
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
 50 55 60  
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
 65 70 75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe		80	85	90
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr		95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu		110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu		125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser		140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro		155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys		170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys		185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln		200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met		215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu		230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln		245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro		260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu		275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln		290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile		305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val		320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln		335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His		350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr				

365	370	375
Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	
380	385	390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	
395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	
410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	
425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	
440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	
455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	
470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	
485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	
500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	
515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	
530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	
545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	
560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	
575	580	585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	
590	595	600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	
605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	
620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	
635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	
650	655	660

Met	Arg	Leu	Gln	Ala	Arg	Gly	Gly	Pro	Ser	Pro	Leu	Lys	Ser	Asn
				665					670					675
Ser	Asp	Ser	Ala	Arg	Leu	Pro	Ile	Ser	Ser	Gly	Ser	Thr	Ser	Ser
				680					685					690

Ser Arg Ile

<210> 484  
 <211> 516  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 68, 70, 84, 147  
 <223> unknown base

<400> 484  
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 ctgccttgca gaggaaanct tcgggactac acctcaagt gcacatgaac 100  
 ctgctgctgg ccgtcttctt gctggacacg agcttctctg tcagcgnagc 150  
 cggtgccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200  
 cctgcacttc tctgtctcac ctgcctttcc tggatgggcc tcgaggggta 250  
 caacctctac cgactcgtgg tggaggtctt tggcaacctat gtccctgget 300  
 acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350  
 acgctggtgg ccttggtgga tgtggacaac tatggcccca tcatcttggc 400  
 tgtgcatagg actccagagg gcgtcatcta cccttccatg tgetggatcc 450  
 gggactccct ggctagctac atcaccaacc tgggcctctt cagcctggtg 500  
 tttctgttca acatgg 516

<210> 485  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 485  
 ggcattggag cagtgtggtg tg 22

<210> 486  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 486  
tggaggccta gatgcggctg gacg 24

<210> 487  
<211> 2849  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2715  
<223> unknown base

<400> 487  
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ggttcaggtc caggttttgc tttgatcctt ttcaaaaact ggagacacag 100  
aagagggctc taggaaaaag ttttggatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttcacccc cagtgcagcc 200  
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250  
ccgccgtgag tgagctctca cccagtcag ccaaagagc ctcttcgggc 300  
ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350  
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400  
cggagtacaa gacctcagc atgagagaat tattactgtg tctactaatg 450  
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500  
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gtttgatgaa agatttgggc ttgaagaccc agaagatgac atatgcaagt 600  
atgattttgt agaagttgag gaaccagtg atggaactat attagggcgc 650  
tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700  
aattaggata agatttgtat ctgatgaata tttccttct gaaccagggt 750  
totgcatcca ctacaacatt gtcatgccac aattcacaga agctgtgagt 800  
ccttcagtcg tacccttctc agctttgcca ctggacctgc ttaataatgc 850  
tataactgcc tttagtagct tggaagacct tattcgatat cttgaaccag 900  
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cttggcaagg cttttgtttt tggaagaaaa tccagagtgg tggatctgaa 1000  
ccttctaaca gaggaggtaa gattatacag ctgcacacct cgtaacttct 1050

cagtgtccat aaggaagaa ctaaagagaa ccgataccat tttctggcca 1100  
 ggttgtctcc tggtaaagc ctgtggtggg aactgtgcct gttgtctcca 1150  
 caattgcaat gaatgtcaat gtgtcccaag caaagtact aaaaaatacc 1200  
 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250  
 tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300  
 cagagggagc acaggaggat agccgcatca ccaccagcag ctcttgccca 1350  
 gagctgtgca gtgcagtggc tgattctatt agagaacgta tgcgttatct 1400  
 ccatcettaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450  
 tacagtgcac tctgaaagag gagacatcaa acagaattag gagttgtgca 1500  
 acagctcttt tgagaggagg cctaaaggac aggagaaaag gtcttcaatc 1550  
 gtggaaagaa aattaaatgt tgtattaaat agatcaccag ctagtctcag 1600  
 agttaccatg tacgtattcc actagctggg ttctgtattt cagttctttc 1650  
 gatacggcct agggtaatgt cagtacagga aaaaaactgt gcaagtgagc 1700  
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 aaatcgtata aaatctggat tttttttttt ttttttgctc atattcacat 1800  
 atgtaaacca gaacattcta tgtactacaa acctggtttt taaaaaggaa 1850  
 ctatgttgct atgaattaaa cttgtgtcat gctgatagga cagactggat 1900  
 ttttcatatt tcttattaaa atttctgcca tttagaagaa gagaactaca 1950  
 ttcattggtt ggaagagata aacctgaaaa gaagagtggc cttatcttca 2000  
 ctttatcgat aagtcagttt atttgtttca ttgtgtacat ttttatattc 2050  
 tccttttgac attataactg ttggcttttc taatcttggt aaatatatct 2100  
 atttttacca aaggatatta atattctttt ttatgacaac ttagatcaac 2150  
 tatttttagc ttggtaaatt tttctaaaca caattgttat agccagagga 2200  
 acaaagatga tataaaatat tgttgctctg acaaaaatac atgtatttca 2250  
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 tggaatagaa ttggtaagtt gcaaagactt ttgaaaata attaaattat 2350  
 catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400  
 aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450  
 atctgagcct agctcagaaa aacataaagc acctgaaaa agacttgga 2500



**SECRET**

<211> 345

<213> Homo sapiens

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly
1				5				10					15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys
				20					25				30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro
				35					40				45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His
				50					55				60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val
				65					70				75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr
				80					85				90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys
				95					100				105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile
				110					115				120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile
				125					130				135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr
				140					145				150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met
				155					160				165
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser
				170					175				180
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser
				185					190				195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
				320					325					330	
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
				335					340					345	

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tcctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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gacctctaca ttccattttg gaagaagact aaaaatggtg tttccaatgt 100

ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200

tctggatggt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250

tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300

accattaacc acataccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400  
 ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa aaccagaagc 450  
 tttagtggac tcacttattt aaaatccctt tacctggatg gaaaccagct 500  
 actagagata ccgcagggcc tccgcctag cttacagctt ctcagccttg 550  
 aggccaacaa catcttttcc atcagaaaag agaacttaac agaactggcc 600  
 aacatagaaa tactctacct gggccaaaac tggtattatc gaaatccttg 650  
 ttatgtttca tattcaatag agaaagatgc cttcctaaac ttgacaaagt 700  
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 aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850  
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 tgtaaaaata attctccctt acagatccct gtaaatgctt ttgatgcgct 950  
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 cccaagatg gttaagaac atcaacaaac tccaggaact ggatctgtcc 1050  
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ggctctgtgg gagttctgtc cttgagtggc caacaaaccc gcaagctcac 3150  
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ggcctatagt caggtgttca aggaacgggt ctagcccttc tttgcaaaac 3250

100-443887-101

<211> 1049

<213> Homo sapiens

<400> 496

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Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser  
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile  
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp  
245 250 255



Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val
				560					565					570
Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile
				575					580					585
Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys
				590					595					600
Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr
				605					610					615
Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His
				620					625					630
Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	Leu
				635					640					645
Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn
				650					655					660
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro
				665					670					675
Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe
				680					685					690
Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp
				695					700					705
Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn
				710					715					720
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile
				725					730					735
Arg	Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg
				740					745					750
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr
				755					760					765
Ser	Phe	Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu
				770					775					780
His	His	Asn	Arg	Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val
				785					790					795
Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr
				800					805					810
Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val
				815					820					825
Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu
				830					835					840



Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

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 <211> 4199  
 <212> DNA  
 <213> Homo sapiens

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 <211> 1041  
 <212> PRT  
 <213> Homo sapiens

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 Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val  
 35 40 45  
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

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Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75
Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90
Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105
Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120
Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135
Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150
Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165
Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180
Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195
Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210
Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
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Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240
Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly
				245					250					255
Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys
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Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn
				275					280					285
Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg
				290					295					300
Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val
				305					310					315
Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Val	Ser	Gly
				320					325					330
Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser
				335					340					345

361

05978295 . 101501

Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile	Ser
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Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu	Arg
365	370	375	
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro	Leu
380	385	390	
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn	Phe
395	400	405	
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn	Leu
410	415	420	
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val	Lys
425	430	435	
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg	His
440	445	450	
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His	Ser
455	460	465	
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys	Ala
470	475	480	
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe	Phe
485	490	495	
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys	Leu
500	505	510	
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr	Glu
515	520	525	
Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn	Asn
530	535	540	
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545	550	555	
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560	565	570	
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575	580	585	
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu	Thr
590	595	600	
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605	610	615	
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620	625	630	
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp

635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu 650 655 660		
Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met 665 670 675		
Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu 680 685 690		
Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp 695 700 705		
Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser 710 715 720		
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val 725 730 735		
Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr 740 745 750		
Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser 755 760 765		
Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile 770 775 780		
Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile 785 790 795		
Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg 800 805 810		
Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp 815 820 825		
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr 830 835 840		
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp 845 850 855		
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr 860 865 870		
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser 875 880 885		
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu 890 895 900		
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu 905 910 915		
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp 920 925 930		

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val  
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 Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe  
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 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile  
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 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu  
 980 985 990  
 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro  
 995 1000 1005  
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn  
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 499

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<210> 500

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 500

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<210> 501

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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 <211> 273  
 <212> PRT  
 <213> Homo sapiens

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<400> 507

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<210> 508  
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<212> PRT  
<213> Homo sapiens

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Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45  
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60  
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75  
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90  
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105  
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120  
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135  
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150  
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165  
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180  
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195  
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
				260					265					270

Lys Asp Ser

<210> 509  
 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

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 ctgaggcccc agcaagggct aggggtccatc tccagtccca ggacacagca 150  
 gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200  
 accggggagg cacaggtggc cccaccacc cggaggagca gctcctgccc 250  
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 gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500  
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 ctgctgcttg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln

140	145	150
Arg Cys Val Asn Thr Ala Gly Ser Tyr	Trp Cys Gln Cys Trp Glu	
155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys Gly	
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser Ala	
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu Leu	
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu Ala	
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu Leu	
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser Glu	
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys Lys	
260	265	270

Lys Asp Ser

- <210> 511
- <211> 21
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 511
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- <210> 512
- <211> 22
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 512
- ttttccactc ctgtcgggtt gg 22
- <210> 513
- <211> 46
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe



<400> 513  
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<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
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ccgacgtgat tccctgggac ggtccgttcc ctgccgtcag ctgccggccc 150  
agttgggtct ccgtgtttca ggccggctcc cccttctctg tctcccttct 200  
cccgtgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350  
cattttggag caggaattcc aatcatgtct gtgatgggtg tgagaaagaa 400  
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atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500  
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atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg cccottgccc 1250  
cccagtgtgc tggatcgaag gggatattttg ccaactggagg aaagtggaag 1300  
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230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 tttggctttg gactctcnct ttctcccaca gacncttcg accatcactg 150  
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
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<210> 517  
 <211> 24  
 <212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 517  
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<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 518  
gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519  
agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 520  
ctcacctgaa atctctcata gccc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

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 <211> 344  
 <212> PRT  
 <213> Homo sapiens

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				20					25					30
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val
				35					40					45
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp
				50					55					60
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu
				65					70					75
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu
				80					85					90
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val
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Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp
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Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser
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Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly
				140					145					150
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro
				155					160					165
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val
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Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln
				185					190					195
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro
				200					205					210
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile
				215					220					225
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr





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cagcgaaatc cggaccgcat ttgaggaggc cctgggacag ctggtttgga 1450  
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Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro
				50					55					60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly
				65					70					75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp
				80					85					90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu
				95					100					105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp
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Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe
				125					130					135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu
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Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro
				155					160					165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly
				170					175					180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala
				185					190					195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala
				200					205					210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser
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Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala
				230					235					240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu
				245					250					255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met
				260					265					270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val
				275					280					285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met
				290					295					300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu
				305					310					315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser

320										325					330	
Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp		Tyr	Leu	Gln	Gln	Val	Ser	
				335						340						345
Glu	Leu	Ile	Asn	Arg	Thr	Glu	Pro	Ser		Ile	Leu	Asn	Asn	Tyr	Leu	
				350						355						360
Ile	Trp	Asn	Leu	Val	Gln	Lys	Thr	Thr		Ser	Ser	Leu	Asp	Arg	Arg	
				365						370						375
Phe	Glu	Ser	Ala	Gln	Glu	Lys	Leu	Leu		Glu	Thr	Leu	Tyr	Gly	Thr	
				380						385						390
Lys	Lys	Ser	Cys	Val	Pro	Arg	Trp	Gln		Thr	Cys	Ile	Ser	Asn	Thr	
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Asp	Asp	Ala	Leu	Gly	Phe	Ala	Leu	Gly		Ser	Leu	Phe	Val	Lys	Ala	
				410						415						420
Thr	Phe	Asp	Arg	Gln	Ser	Lys	Glu	Ile		Ala	Glu	Gly	Met	Ile	Ser	
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Glu	Ile	Arg	Thr	Ala	Phe	Glu	Glu	Ala		Leu	Gly	Gln	Leu	Val	Trp	
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Met	Asp	Glu	Lys	Thr	Arg	Gln	Ala	Ala		Lys	Glu	Lys	Ala	Asp	Ala	
				455						460						465
Ile	Tyr	Asp	Met	Ile	Gly	Phe	Pro	Asp		Phe	Ile	Leu	Glu	Pro	Lys	
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Glu	Leu	Asp	Asp	Val	Tyr	Asp	Gly	Tyr		Glu	Ile	Ser	Glu	Asp	Ser	
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Phe	Phe	Gln	Asn	Met	Leu	Asn	Leu	Tyr		Asn	Phe	Ser	Ala	Lys	Val	
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Met	Ala	Asp	Gln	Leu	Arg	Lys	Pro	Pro		Ser	Arg	Asp	Gln	Trp	Ser	
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Met	Gly	His	Glu	Leu	Thr	His	Ala	Phe		Asp	Asp	Gln	Gly	Arg	Glu	
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Tyr	Asp	Lys	Glu	Gly	Asn	Leu	Arg	Pro		Trp	Trp	Gln	Asn	Glu	Ser	
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Leu	Ala	Ala	Phe	Arg	Asn	His	Thr	Ala		Cys	Met	Glu	Glu	Gln	Tyr	
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Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
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Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
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Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
				695					700					705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
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Trp

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 <213> Homo sapiens  
  
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 <222> 1478, 3978, 4057-4058, 4070  
 <223> unknown base

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 agcctcccg ccccgccggc cccgctgctg ctctcggggc tgctgctgct 150  
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 <213> Homo sapiens

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 cagagaccca tcccacagca cctgccttac agaggcctgc attcagtggt 350



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 <213> Homo sapiens

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 gagtccctgg cagccttccg gaaccacacg gcctgcatgg aggaacagta 250  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 24

<212> DNA

<213> Artificial Sequence

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**SECRET**

<223> Synthetic oligonucleotide probe

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<211> 23

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

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<211> 24

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

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<211> 23

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<211> 19

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<223> Synthetic oligonucleotide probe

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<211> 25

<213> Artificial Sequence

394

SECRET (S) (U)

cgactccctg agcgagcaga tttcc 25

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

gctgggcagt cacgagtctt 20

<213> Artificial Sequence

**<223> Synthetic oligonucleotide probe**

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<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

tgggccaagg gctgc 15

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

<400> 557

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<210> 558

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 558

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<210> 559

<211> 24

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<210> 562

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<210> 582  
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<400> 585

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<210> 586

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<223> Synthetic oligonucleotide probe

<400> 586

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<210> 587

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**SECRET**

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<223> Synthetic oligonucleotide probe

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<211> 25

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<211> 28

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<210> 598

<211> 23

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<210> 611  
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 <212> PRT  
 <213> Homo Sapien

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 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn  
 35 40 45  
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu  
 50 55 60  
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
 65 70 75  
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
 80 85 90  
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
 95 100 105  
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr  
 110 115 120  
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val  
 125 130 135  
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu  
 140 145 150  
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu  
 155 160 165  
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe  
 170 175 180  
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln  
 185 190 195  
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro  
 200 205 210  
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile  
 215 220 225  
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

230	235	240
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245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile		
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val		
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys		
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr		
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys		
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Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr		
335	340	345
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350		

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 ctgcttttca ccaaattgca atggagcctt togaaatcaa tggtccaaag 200  
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ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850  
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Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu  
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aaaagccaaa atgaaactga tggtagctgt tttcaccatt gggctaactt 200
tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250
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# SECRET

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Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
                      35                      40                      45
Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
                      50                      55                      60
Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
                      65                      70                      75
Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
                      80                      85                      90
Phe Val Ile Pro Cys Asn Asn Gln
                      95

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gggtcccggg aggcgggctc tgctcgccc gagatgtgga atctccttca 200
cgaaaccgac tcggctgtgg ccaccgcgcg cgcgccgcgc tggctgtgcg 250
ctgggggcgt ggtgctggcg ggtggcttct ttctcctcgg ctctctcttc 300
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 tttcagcttg caaagcaaat tcaatcccag tggaaagaat ttggcctgga 500  
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550  
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 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650  
 tattgtacca cctttcagtg ctttctctcc tcaaggaatg ccagagggcg 700  
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 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcaggggccca 850  
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Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
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Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly
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Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly
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Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser
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Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala
				170					175					180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn
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Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg
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Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val
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Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
				230					235					240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg
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Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro
				260					265					270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu
				275					280					285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr
				290					295					300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro
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Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly
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Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His
				335					340					345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly
				350					355					360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly
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Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser

380					385					390				
Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu
				395					400					405
Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser
				410					415					420
Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala
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Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile
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Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
				470					475					480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu
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Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro
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Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe
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Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn
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Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val
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Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe
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Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe
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Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr
				590					595					600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser
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Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp
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Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys
				635					640					645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val
				650					655					660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe
				665					670					675

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
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Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
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